

FIGURE 1A

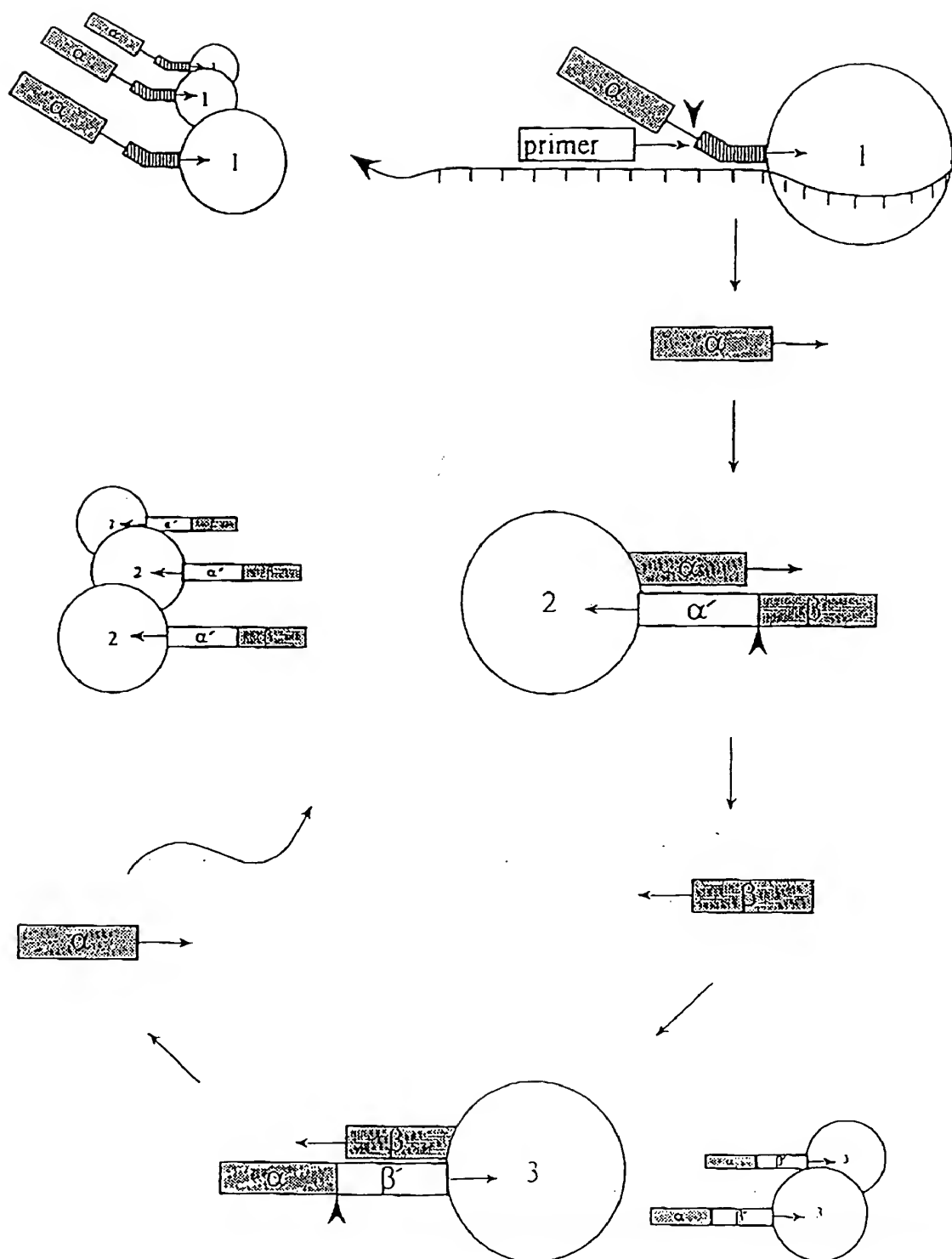
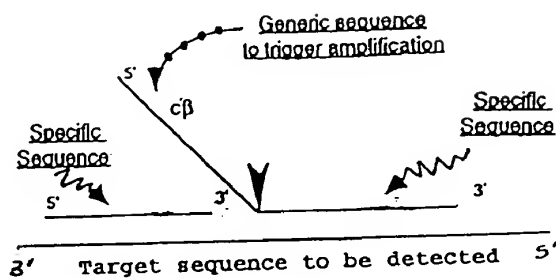


FIGURE 1 B

PART ONE: TRIGGER REACTION



PART TWO: DETECTION REACTION

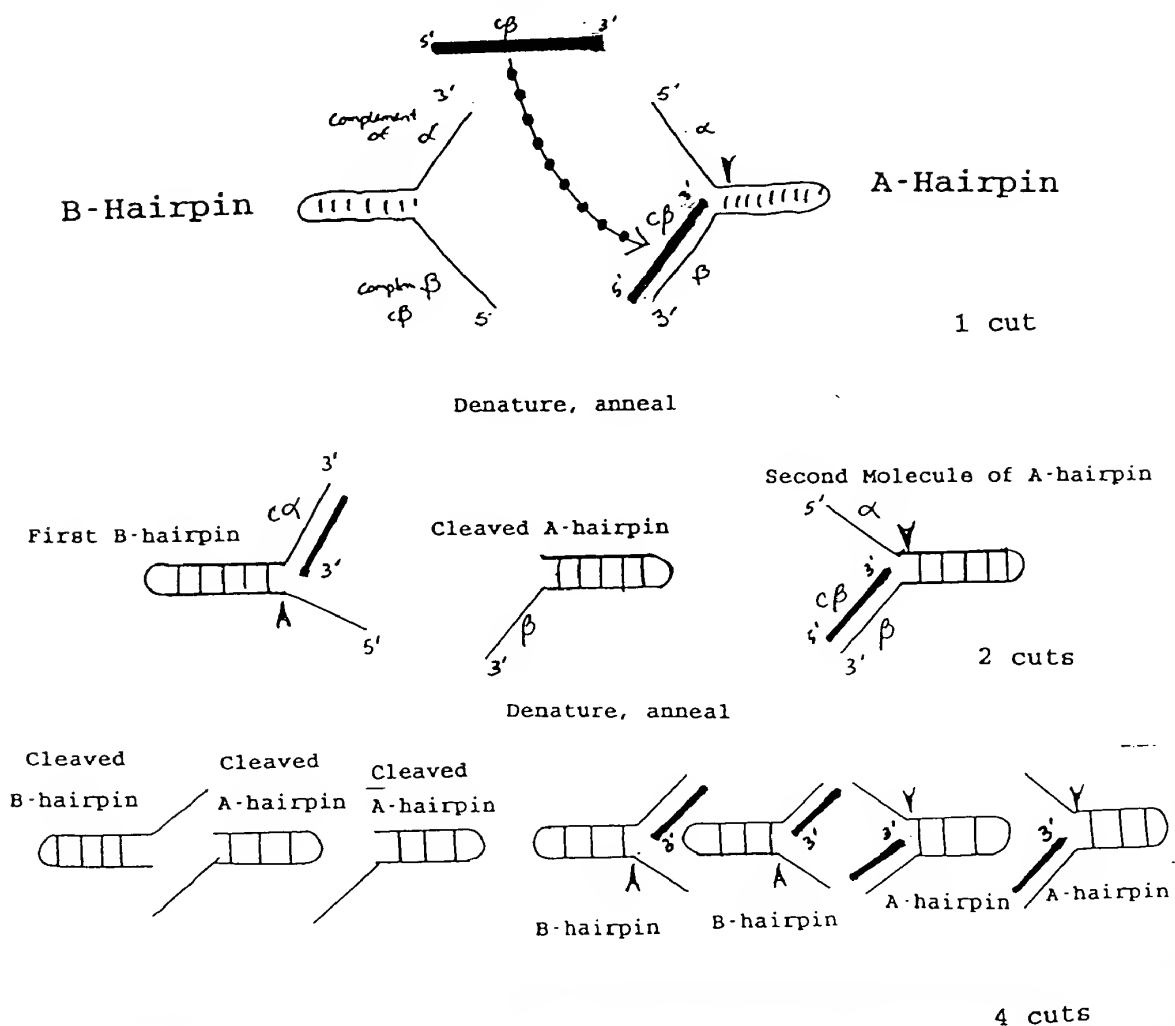


FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	CGAGGGGACGACGTCCTGGCCACCCCTGGCCCAAGAGGGCGAAAGAGGGGTACGAGGTGGCCATCCTC	417
DNAPTAA (SEQ ID NO:1)C.....G.....G.....C.....	414
DNAPTFL (SEQ ID NO:2)G.....GG.....	420
DNAPTTH (SEQ ID NO:3)T.....C.....	
MAJORITY	ACCGGGGACGGGACCTCTACGAGCTCCTTCCGACCCGCATCGCCGTCCTCCAGCCGAGGGGTACCTCA	
DNAPTAA (SEQ ID NO:1)AAA.....T.....CA.....	487
DNAPTFL (SEQ ID NO:2)T.....G.....G.....A.....T.....G.....	484
DNAPTTH (SEQ ID NO:3)A.....G.....G.....G.....CC.....	490
MAJORITY	TCACCCCGGGCGTGGCTTTGGGAGAGTACGGCCCTGAGCCCGGAGGAGTGGGTGGACTACCGGGCGCTGGC	
DNAPTAA (SEQ ID NO:1)C.....A.....C.....C.....CC.....A.....	557
DNAPTFL (SEQ ID NO:2)AC.....C.....C.....C.....T.....G.....C.....T.....	554
DNAPTTH (SEQ ID NO:3)A.....C.....C.....C.....T.....G.....C.....T.....	560
MAJORITY	CGGGGACCCCTCCGACAACTCCCGGGGCTCAAGGGCATCGGGGAGAGAGCGGCCCGAGGCTCCTCXAG	
DNAPTAA (SEQ ID NO:1)GAG.....T.....GAG.....T.....GG.....	627
DNAPTFL (SEQ ID NO:2)G.....T.....A.....G.....A.....G.....A.....CGC.....	624
DNAPTTH (SEQ ID NO:3)G.....T.....A.....G.....T.....A.....A.....	630
MAJORITY	GAGTGGGGGAGGCTGGAAAAAGCTCCTCAAGAACCTGGACCGGGTGAAGCCCGC...CXTCGGGGGAGAAGA	
DNAPTAA (SEQ ID NO:1)GC.....C.....A.....	694
DNAPTFL (SEQ ID NO:2)T.....C.....C.....A.....T.....T.....G.....C.....	691
DNAPTTH (SEQ ID NO:3)A.....A.....A.....A.....A.....A.....G.....	700

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	TCCAGGGCCACATGGAXGACCTGAXGCTCTCCTGGGAGCTXTCCAGGCTGGGACGGACCTGCCCGCTGGA	
DNAPTAD (SEQ ID NO:1)	...T.....C..T...A.....C..GG..A.....	764
DNAPTFL (SEQ ID NO:2)	...GGG...G.C..GCC..T...G..A...T.....A...T.....	761
DNAPTTH (SEQ ID NO:3)	...A.....C.....A.....C.G.....T.....C.....G.....C.....	770
MAJORITY	GCTGGACTTCGCCAAGXGGCGGAGACCGGAGCGGGCTTAGGGCTTTCTGGAGAGGCTGGAGTTT	
DNAPTAD	...AA.....A.....A.....T.....T.....T.....	834
DNAPTFL	...GG.G.C.C.C.CACA...A...T.....T..GC...T...T.....C..T.....	831
DNAPTTH	...C.....C..G.....C.....C.....C.....	840
MAJORITY	GGCAGCCTCCTCCACGAGTTCGGCCCTCCTGGAGGGGGCCCAAGGGCCTGGAGGAGGGCCCTGCCCGCCCGG	
DNAPTAD	...T.....T.....AA.....	904
DNAPTFL	...A.....G..G.....G.GA.....T.....	901
DNAPTTH	...C.....GCGG.....	910
MAJORITY	CGGAAGGGCCCTTCGTGGGCTTTGTCCTTTCCCGCCCGGAGCCCAATGTGGCGCGAGCTTCTGCCCGCTGGC	
DNAPTAD	...G.....AAG.....T.....	974
DNAPTFL	...T..TT.....TC.T.....T.....	971
DNAPTTH	...C.....C.....G.....AAA.....	980
MAJORITY	CGCGGGCCAGGGCGCGGCTCCACCGGGGACGACGCGCTTAXGGGCGCTXAGGGACCTXAAGGAGCTG	
DNAPTAD	...G.....C..C..G..T.A..AA.C..C.....G.....C..	1044
DNAPTFL	...T.GG...GT...G..CC...T.....A.....C..G.....G.....T.....G.....	1041
DNAPTTH	...TG...C.....G.....GCG...G..A.A.....C.....C.....	1050

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	GGAGATCCGCGCGCCTCGAGGAGGAGGTCTTCCGGCCTGGCGCGGCACCCCTTCAACCTCAACTCCCGGGGAC	
DNAPTAA (SEQ ID NO:1)GC.....CC.....	1464
DNAPTFL (SEQ ID NO:2)	...G.G...AG..G.....	1461
DNAPTTH (SEQ ID NO:3)T.....G.....	1470
MAJORITY	CAGCTGGAAAGCGTGCTCTTTGACGAGCTXGGGCTTCCCGGCCATCGGCAAGACGGAGACXGGCAAGC	
DNAPTAA (SEQ ID NO:1)C.....A.....	1534
DNAPTFL (SEQ ID NO:2)	...GC.....G..C..G..T.....	1531
DNAPTTH (SEQ ID NO:3)TA.....T.G..G.....	1540
MAJORITY	GCTCCACCAGCGCGCGTGCTGGAGGCCCTXCGXGAGGCCACCCCATCGTGGAGAAAGATCCTGCAGTA	
DNAPTAA (SEQ ID NO:1)C.....C..C.....	1604
DNAPTFL (SEQ ID NO:2)	...T.....G..A.....CGGC.....	1601
DNAPTTH (SEQ ID NO:3)G.....A..G.....	1610
MAJORITY	CGGGGAGCTCAGCAAGCTCAAGAACACCTACATXGACCCCTGCCXGXCCTCCTCCACCCGAGGACGGGGC	
DNAPTAA (SEQ ID NO:1)G.....G.....T.....G.A...A.....	1674
DNAPTFL (SEQ ID NO:2)A.....A.....C.C...G.....A...C.....	1671
DNAPTTH (SEQ ID NO:3)G.G.....C..AAG.....G.....	1680
MAJORITY	CGCCTCCACACCGCGCTCAACGAGACGGCCACGGCCAGGGCTAGTAGCTCCGACCCCAACCTGC	
DNAPTAA (SEQ ID NO:1)A.....T.....	1744
DNAPTFL (SEQ ID NO:2)G.....C.....TCC.....	1741
DNAPTTH (SEQ ID NO:3)G.....	1750

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	AGAACATCCCGCTCCGCCACCCXCTGGGCCAGAGGATCCGGCCGGGCTTCGTGGCCGAGGAGGGTGGGT	
DNAPTAO (SEQ ID NO:1)G..T..G.....A..C.....G...C..	1814
DNAPTFL (SEQ ID NO:2)G.....T.....C..C.....A.....C.....	1811
DNAPTTH (SEQ ID NO:3)CT.....C.....T.....C.....T.....C..	1820
MAJORITY	GTGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGGTCTCGCCCCACCTCTCCGGGGGAGGAGAACCTG	
DNAPTAO	A.....T.....T.....A.....G.....C.....	1884
DNAPTFLT..T.....C.....T.....T.....C.....	1881
DNAPTTHT.....C.....C.....C.....A.....	1890
MAJORITY	ATCCGGGTCTTCAGGAGGGAGGACATCCACACCCAGACCCGAGCTGCATGTTCCGGCGTCCCGCCGGG	
DNAPTAOC.....C.....GG.....G...G...G...G...	1954
DNAPTFLT.....T.....T.....T.....T.....T.....	1951
DNAPTTHA.....A.....A.....A.....A.....A.....	1960
MAJORITY	AGCCCGCTGGACCCCGCTGATGGCGCGGGGGGCGAAGACCATCAACTTCGGGGTCCTCTACGGGCATGTCCGGC	
DNAPTAOA..GG..A.....T.....GG..G.....G...G...G...	2024
DNAPTFLA..GG..A.....T.....GG..G.....G...G...G...	2021
DNAPTTHA..GG..A.....T.....GG..G.....G...G...G...	2030
MAJORITY	CCACCGCCCTCTCCACAGGAGCTTCCCATCCCGCTACGAGGAGGGGGTGGCGTTCAATGAGGGGCTACTTCCAG	
DNAPTAOA.....A.....T.....CCA.....T...T...	2094
DNAPTFLGG.....T.....T.....T.....T.....T...	2091
DNAPTTHTA..G.....T.....T.....T.....T.....A..	2100

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	AGCTTCCCCAAAGGTGCGGGCGCTGCATTGAGAAAGACCGCTCGAGGAGGGCAGAGCGCGGGGTACGTGGAGA	2164
DNAPTAA (SEQ ID NO:1)	2161
DNAPTFL (SEQ ID NO:2)	A.....GG.....C.....T.....	2170
DNAPTH (SEQ ID NO:3)A.....A.....G.....A.....C.....A.....	
MAJORITY	CCCTCTTGGGGCGCGCGCGCTACGTGCCCCGACCTCAACGGCGCGGGTGAAGAGCGTCCGGGAGGGCGCGGA	
DNAPTAAC.....A.....AG.G.....C.....	2234
DNAPTFLT.....	2231
DNAPTH	AA.AA.....CA.....C.....	2240
MAJORITY	GGCCATGGCCCTTCAACATGCCCGTCCAGGGCACCGCGCGGACCTCATGAAGCTGGCCATGGTGAAGCTC	
DNAPTAAT.....	2304
DNAPTFLG.....	2301
DNAPTHC.....	2310
MAJORITY	TTCCCCCGCGCTXCAGGAAATGGGGGCCAGGATGCTCCTXCAGGTCCACGAGGAGCTGGTGGTGGAGGGCGC	
DNAPTAA	A.....GG.....T.....	2374
DNAPTFLT.....G.....TT.G.....G.....	2371
DNAPTHC.....G.....C.....C.....G.....	2380
MAJORITY	CCAAAGAGCGGGCGGAGGXGGTGGCGCGCTTGGCCAAAGGAGGTGCTATGGCGCTGGCGGT	
DNAPTAA	A.....A.....CC.....GGG.....G.....	2444
DNAPTFLG.....AC.....A.....GG.....CAG.....	2441
DNAPTHC.....C.....A.....G.....C.....AA.....C.....G.....	2450

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	GGCCCTGGAGGTGGAGGTGGCGATGGGGGAGGACTGGCTCTCGGGCCAAAGGAGTAG	2499
DNAPTAD (SEQ ID NO:1)A.....GA	2496
DNAPTFL (SEQ ID NO:2)CC.....	2505
DNAPTH (SEQ ID NO:3)T.....GT...	

FIGURE 3

MAJORITY (SEQ ID NO:8)	MXAMLPLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEPVQAVYGFAKSLLKALKEDG·DAVXVVFDAK	
TAQ PR0 (SEQ ID NO:4)	RG.....H.....I.....	69
TRL PR0 (SEQ ID NO:5)V.V.....	68
TTH PR0 (SEQ ID NO:6)	E.....YK..F.....	70
MAJORITY	APSFRRHEAYEYKAGRPTPEDFPROLALI KELVDLLGLXRLEVPGYEADDVLATLAKKAEKEGYEVRI L	
TAQ PR0	GG.....A.....S.....	139
TRL PR0V.....F.....R.....	138
TTH PR0FT.....	140
MAJORITY	TADRDLYQLLSDRIAVLHPEGYLITPAWLWEKYGLRPEQWVDYRALXGDPDSNLPQVKGIGECTAXKLLX	
TAQ PR0	K.....H.....D..A...T..E.....R...E 209	
TRL PR0E..I.....Y.....A...I.....QR..IR 208	
TTH PR0V...V.....H...E.....F...V.....L...K 210	
MAJORITY	EWGSLLENLLKNLDRVKP·XXREKIXAHMEDLXLXSLXSXVRTDLPLEVDFAXRRREPDREGLRAFLELEF	
TAQ PR0	A.....L...Al...L...D...K...WD.AK.....K.....R.....	278
TRL PR0FQH..Q...SL...LQ.G..A.A..RK..Q.H.....GR..T.NL.....	277
TTH PR0ENV...K..L...R...LE..R.....L.QG.....	280
MAJORITY	GSLLHEFGLLXPKALEEAPWPPPEGAFVGFVLSRPEPMWAEALLAALAAARXGRVHRAXDPLXGLRDLKEV	
TAQ PR0	S.....K.....D.....G.....PE.YKA.....A 348	
TRL PR0	G...A.....L..SF.....G.WE..L...Q...R.....G. 347	
TTH PR0	A.AP.....K.....C.D.....A...A...K..... 350	

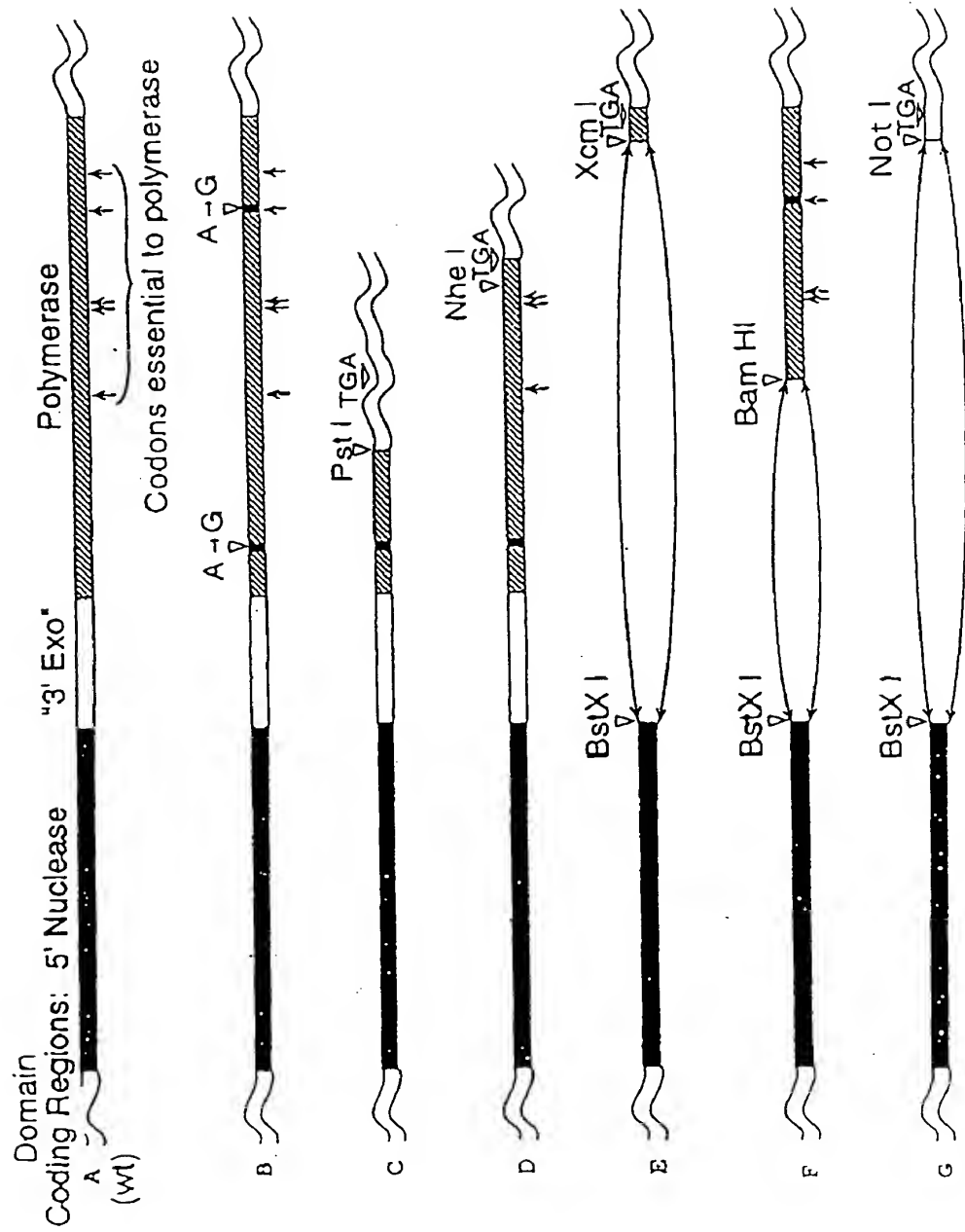
FIGURE 3 (cont'd)

MAJORITY (SEQ ID NO:8)	RGLLAKOLAVLALREGLDLXPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEADAGERALLSERLFXNLXX	
TAQ PRO (SEQ ID NO:4)S.....G.P.....E.....A.....A.....WG	418
TEL PRO (SEQ ID NO:5)I.....F.E.....A.....A.....QT.KE	417
TTH PRO (SEQ ID NO:6)S.....V.....AH.....HR..LK	420
MAJORITY	RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLOALSLEVAEEI RRLEEEVFRLAGHPFNLNSRD	
TAQ PROR...R...A.....R.....A.....A.....	488
TEL PROK.....E.....R.....EA.V.Q.....	487
TTH PROK.....H.....L.....	490
MAJORITY	OLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTCLKNTYIDPLPXLVHPRTG	
TAQ PROS.....S.....D.I.....	558
TEL PRODR.....A.....K..	557
TTH PROR...L...Q.....H.....V.....S.....	560
MAJORITY	RLHTRFNOTATATGRSSDPNLONI PVRTPLGORI RRAFVAEEGWXLVALDYSQIELRVLAHLSGDENL	
TAQ PROI.....L.....	628
TEL PROV.....V.....	627
TTH PROA.....A.....	630
MAJORITY	IRVFOEGRDIHTOTASWMFGVPPEAVDPLMRRAAKTINFGVLYGMSAHLRSQELAI PYEEAVAFIERYFO	
TAQ PROE.....R.....Q.....	698
TEL PROS...G.....G...S.....	697
TTH PROK.....V.....	700

FIGURE 3 (cont'd)

MAJORITY (SEQ ID NO:8)	SFPKVRAWI EKTLEEGRRRGYVETLFGRRRYVVDLNNARVKSUREAAERMAFNMPVOGTAADL MKL AHVKL	
TAQ PR0 (SEQ ID NO:4)E.....	768
TRL PR0 (SEQ ID NO:5)	Y.....G.....	767
TTH PR0 (SEQ ID NO:6)K.....	770
MAJORITY	FPRLXEMGARM L OVHDELVL EAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX	
TAQ PR0E.....	833
TRL PR0Q.L.....	831
TTH PR0R.....	835

FIGURE 4



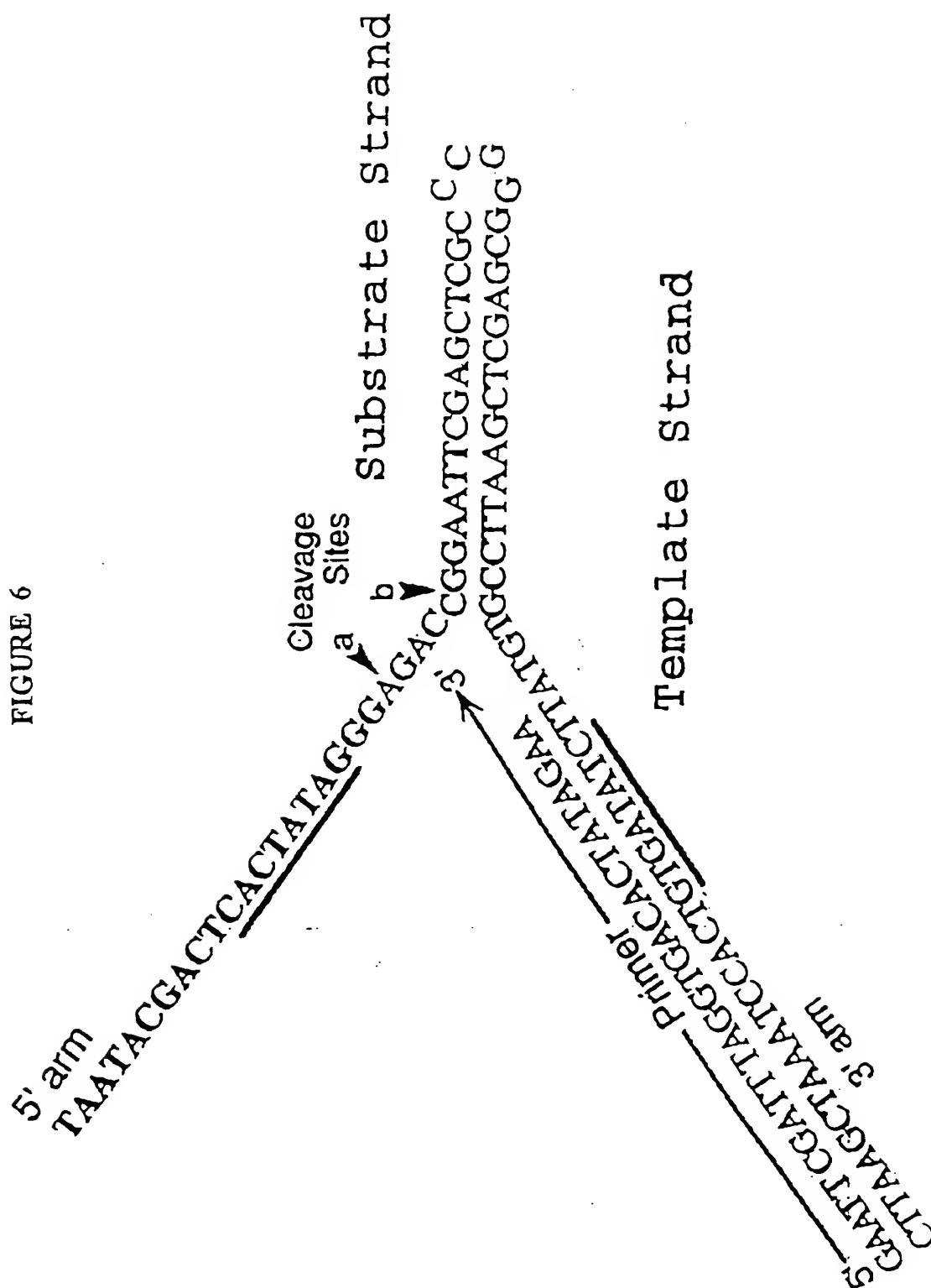


FIGURE 7



FIGURE 8

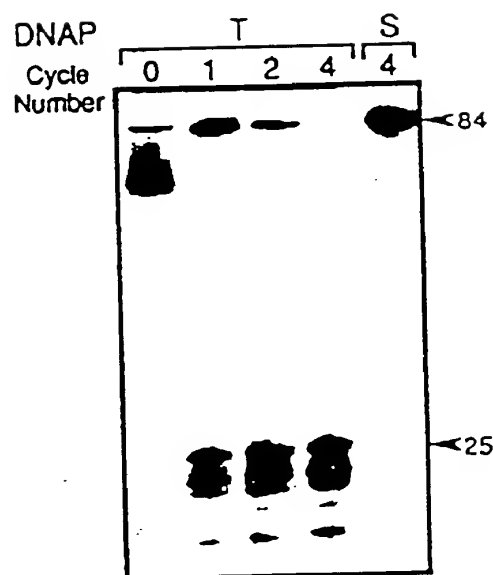


FIGURE 9

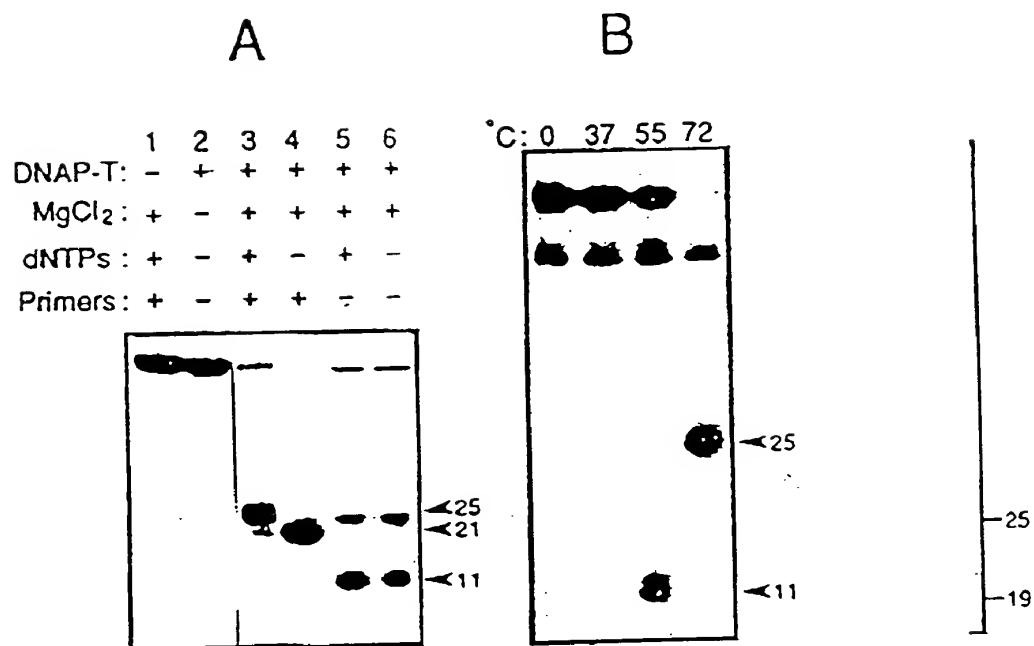


FIGURE 10

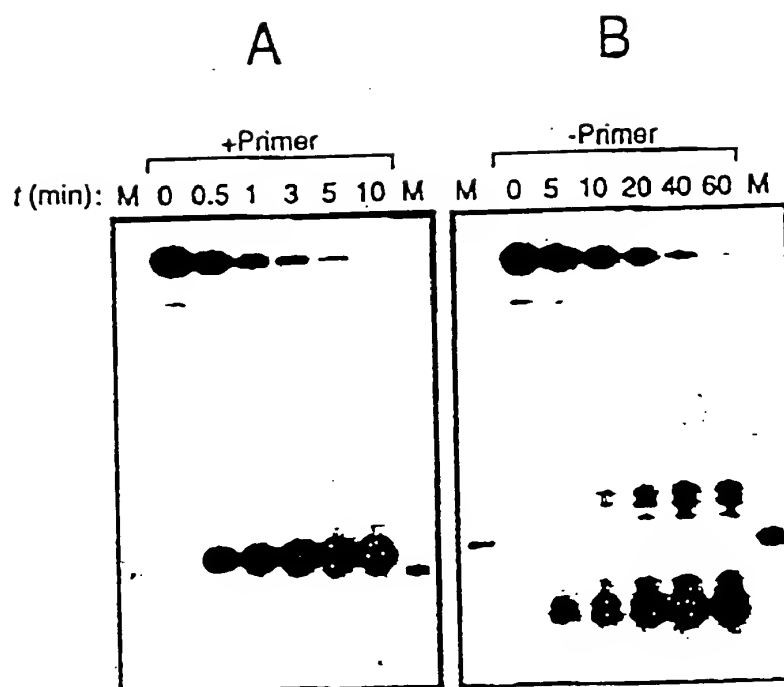


FIGURE 12

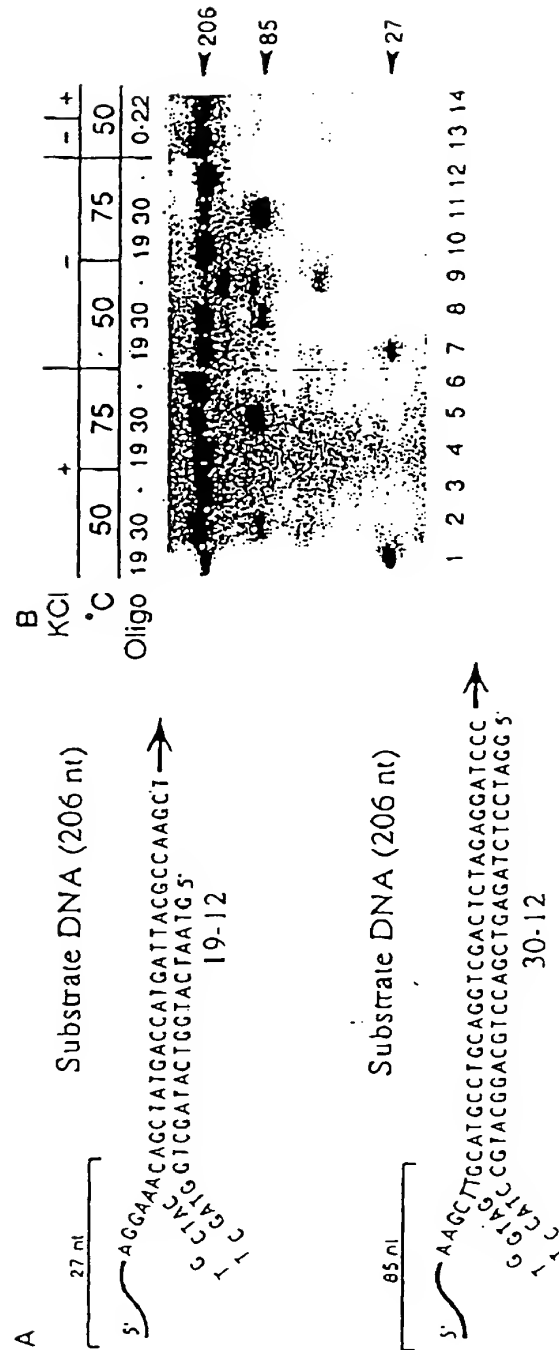


FIGURE 13

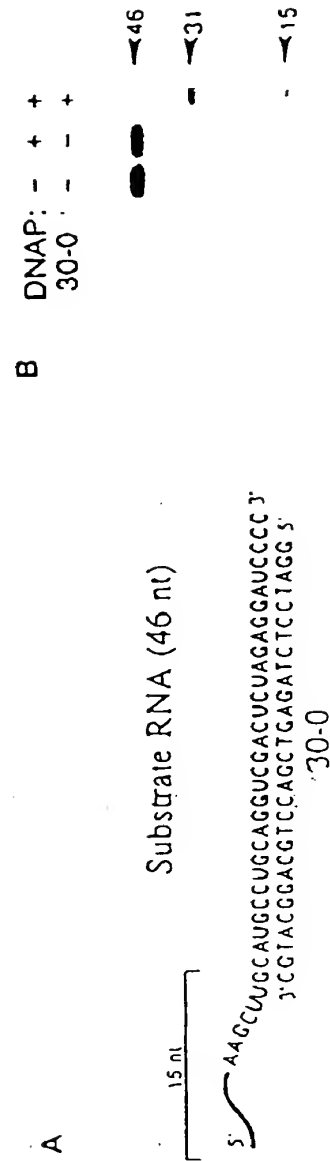


FIGURE 14

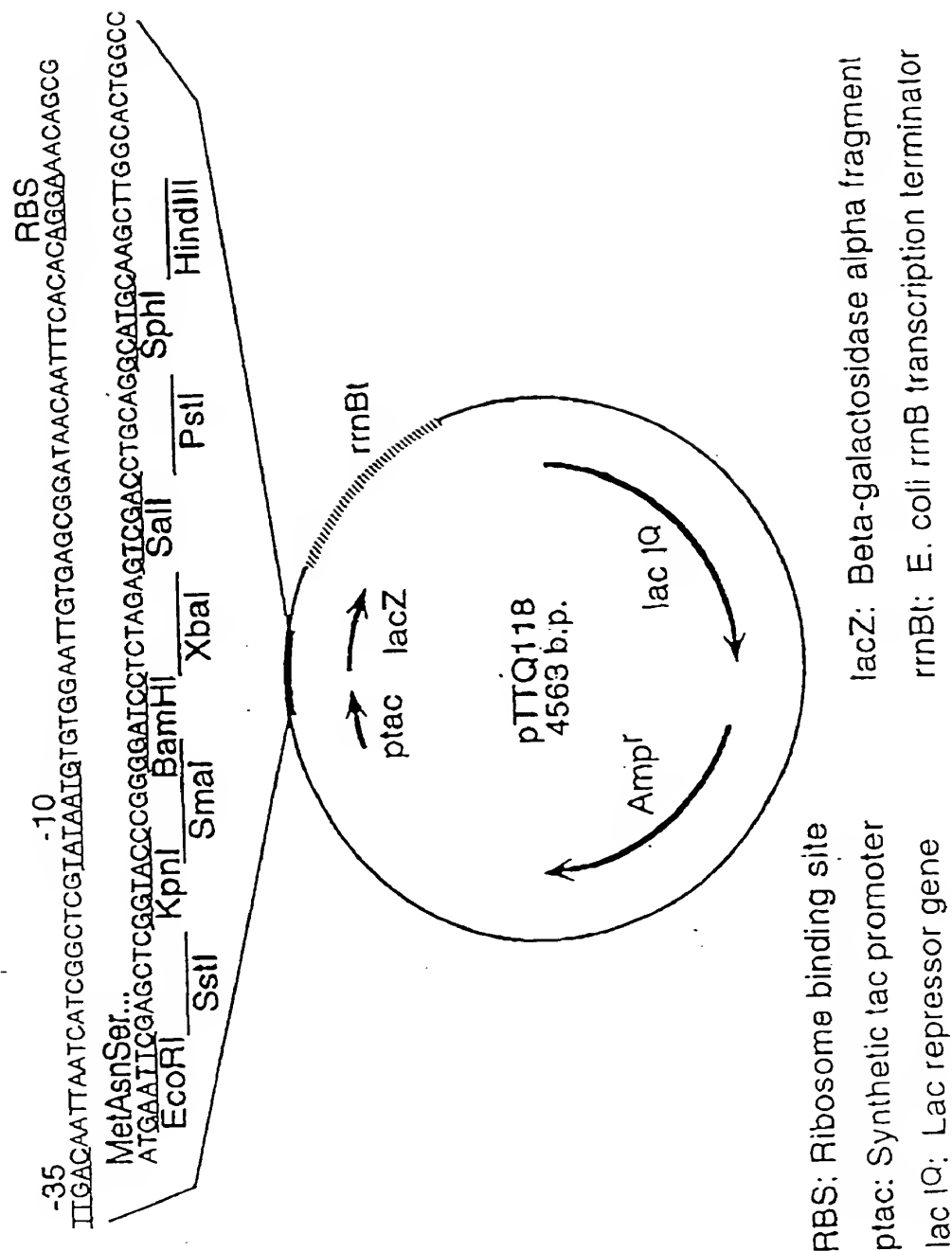
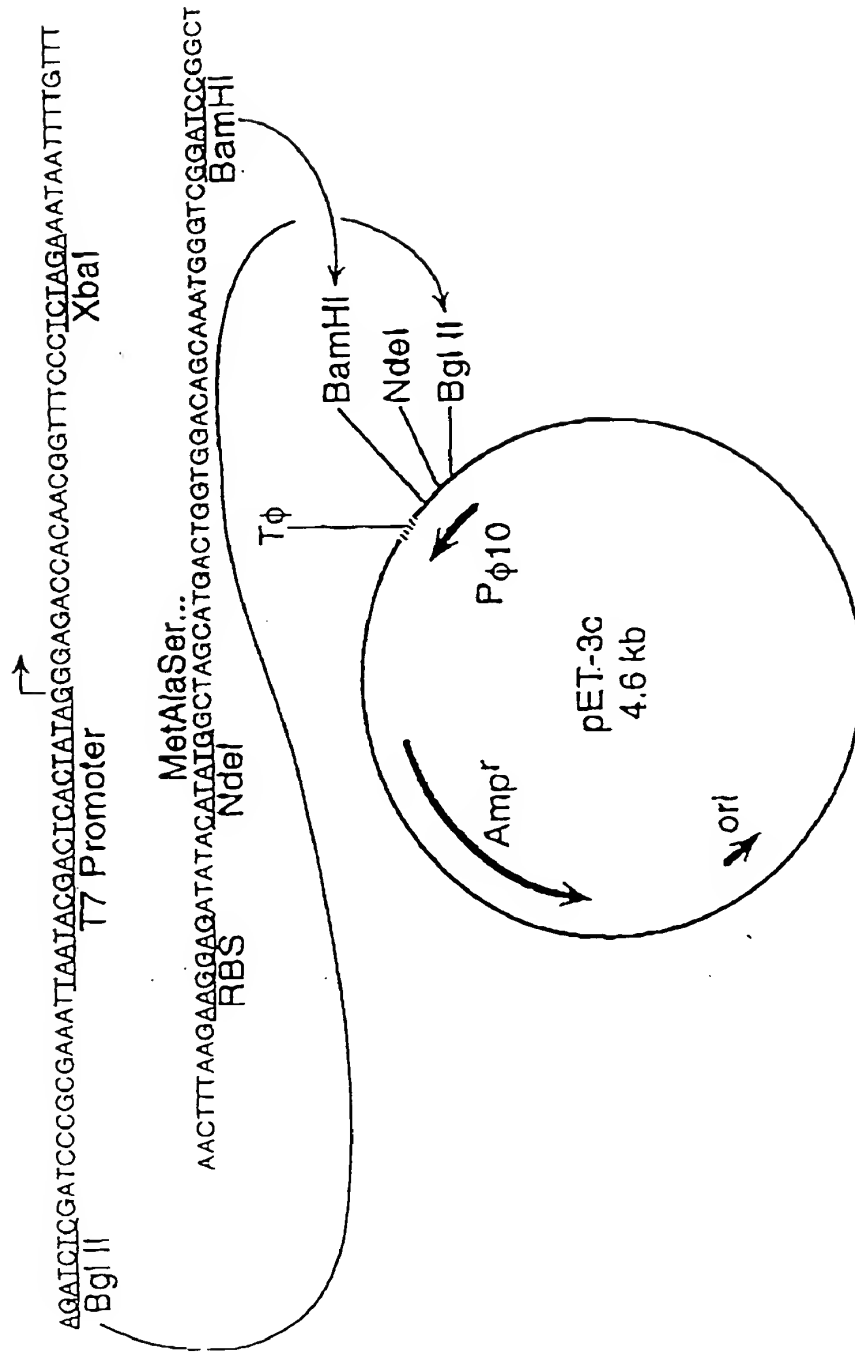


FIGURE 15



RBS: Ribosome binding site

P ϕ 10: Bacteriophage T7 ϕ 10 promoterT ϕ : T7 ϕ Terminator

FIGURE 16

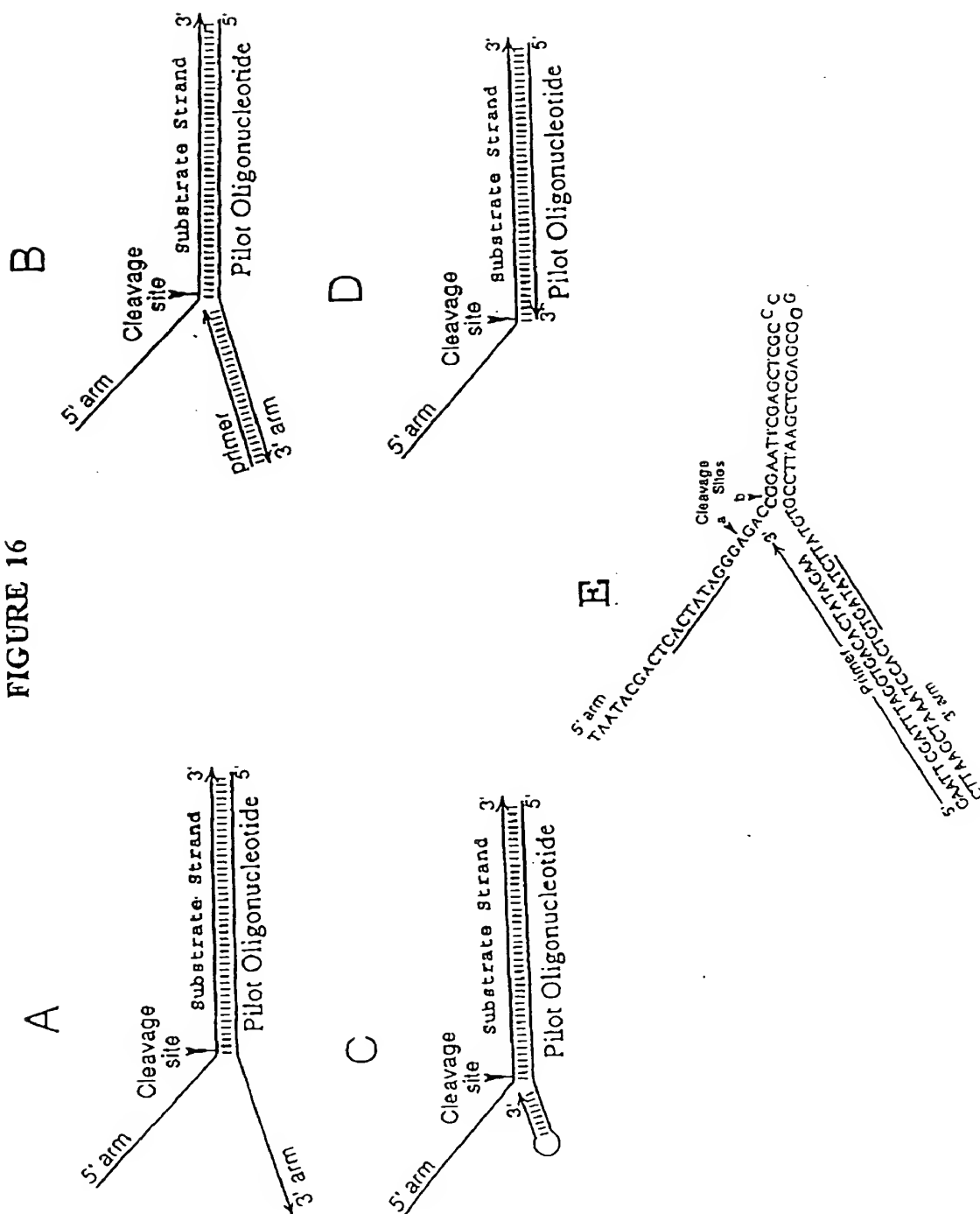
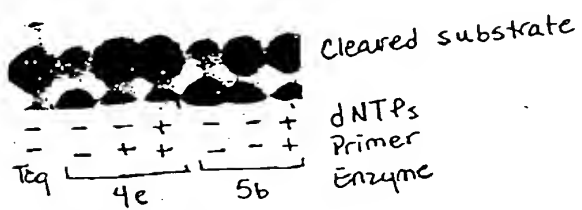
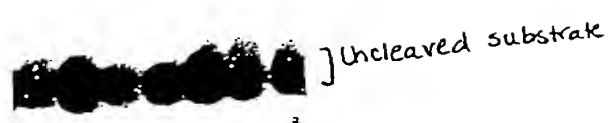
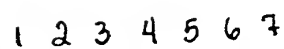


FIGURE 17



dNTPs
Primer
Enzyme

FIGURE 18

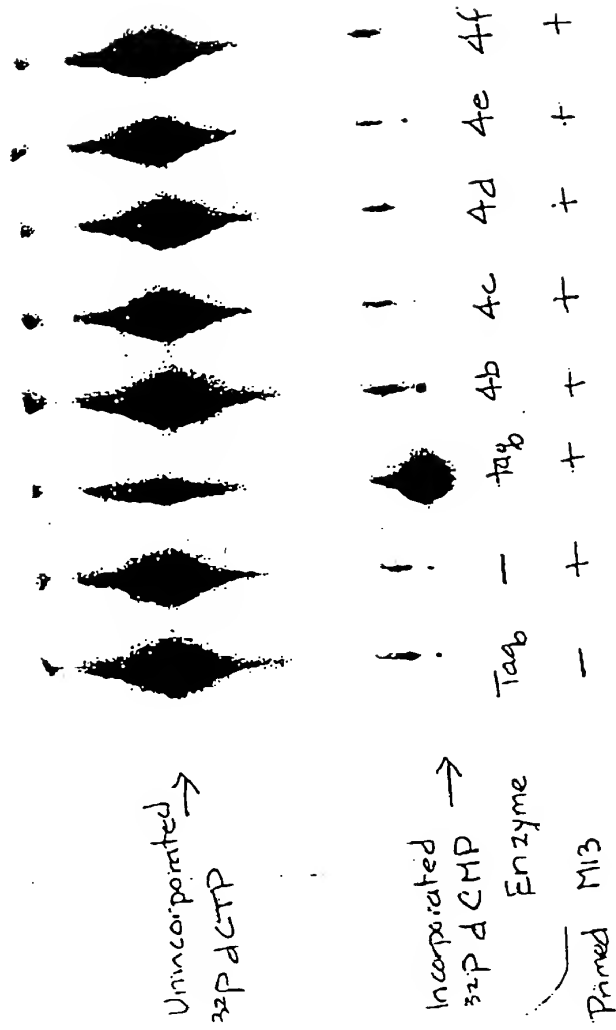
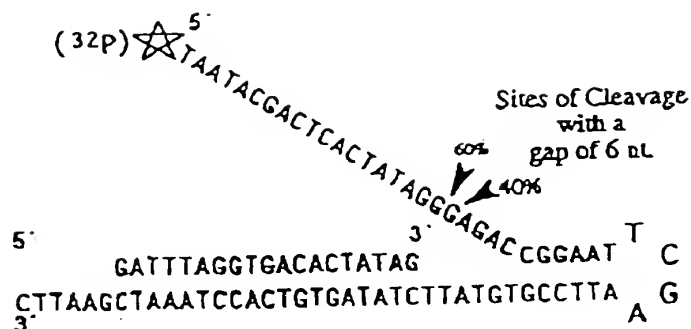


FIGURE 19

A



B

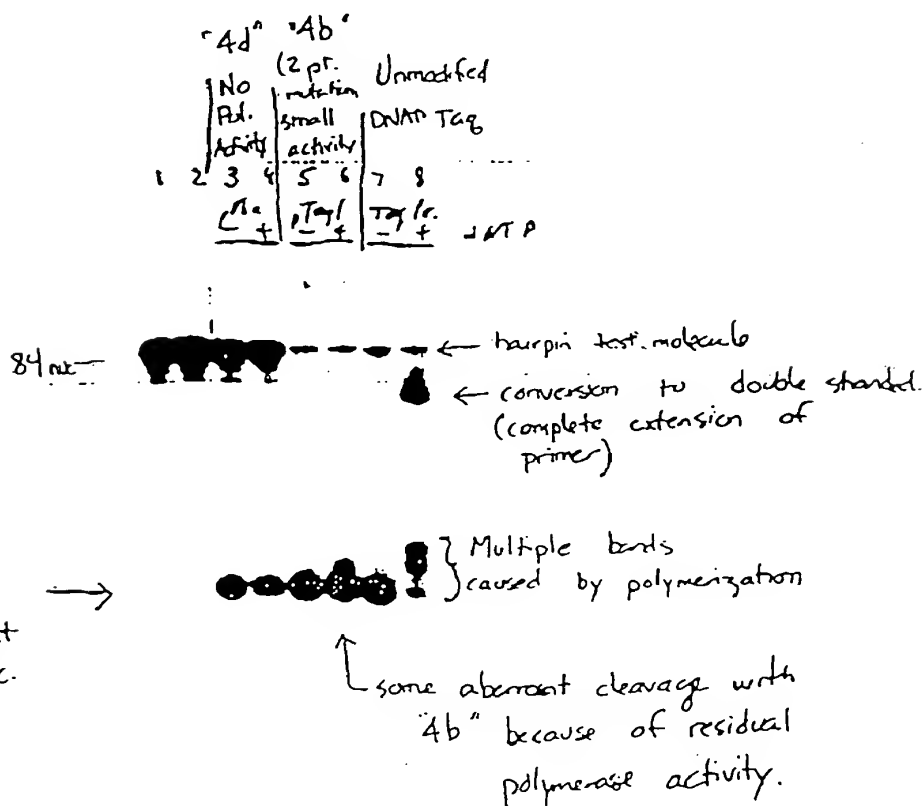


FIGURE 21

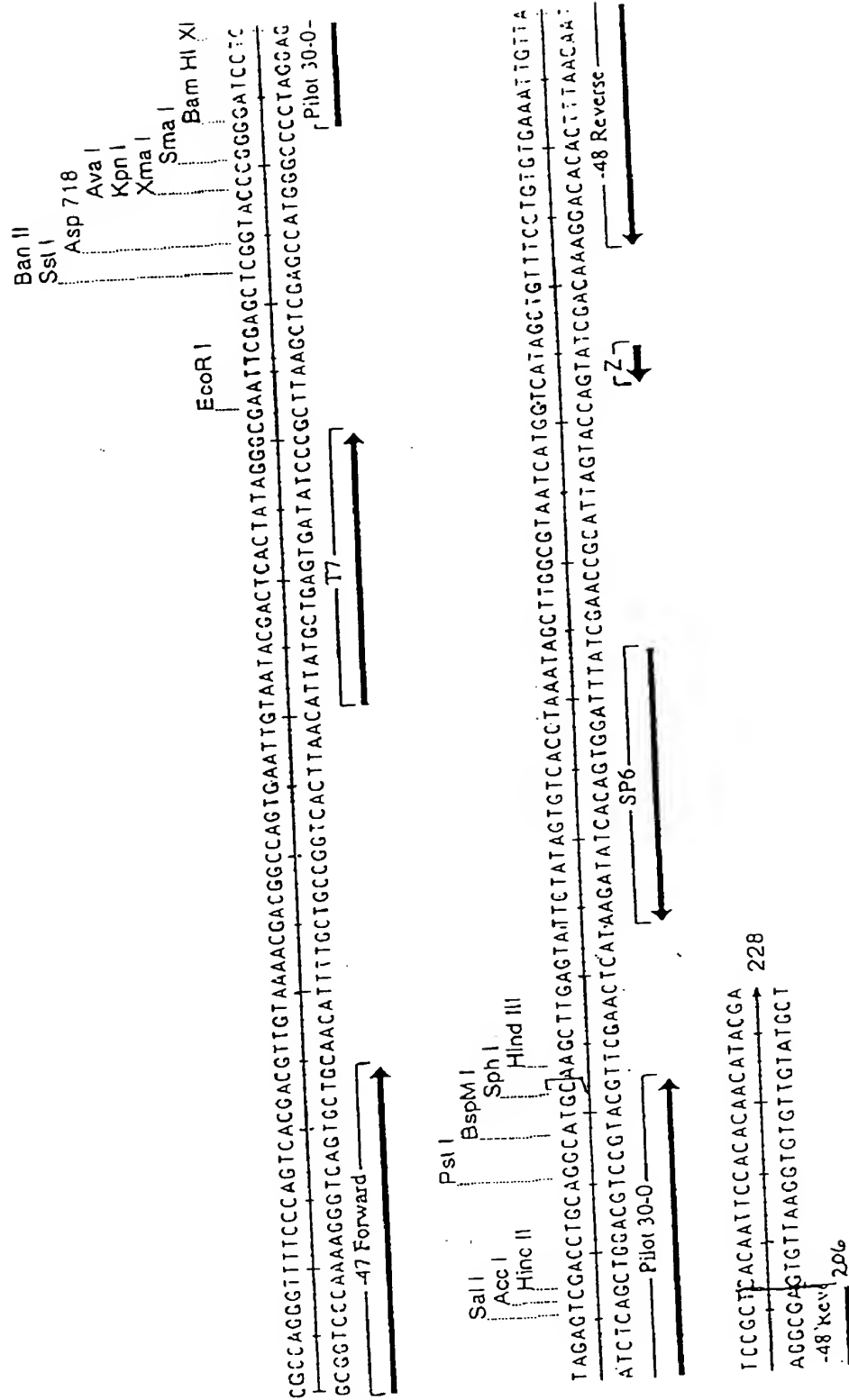


FIGURE 22A

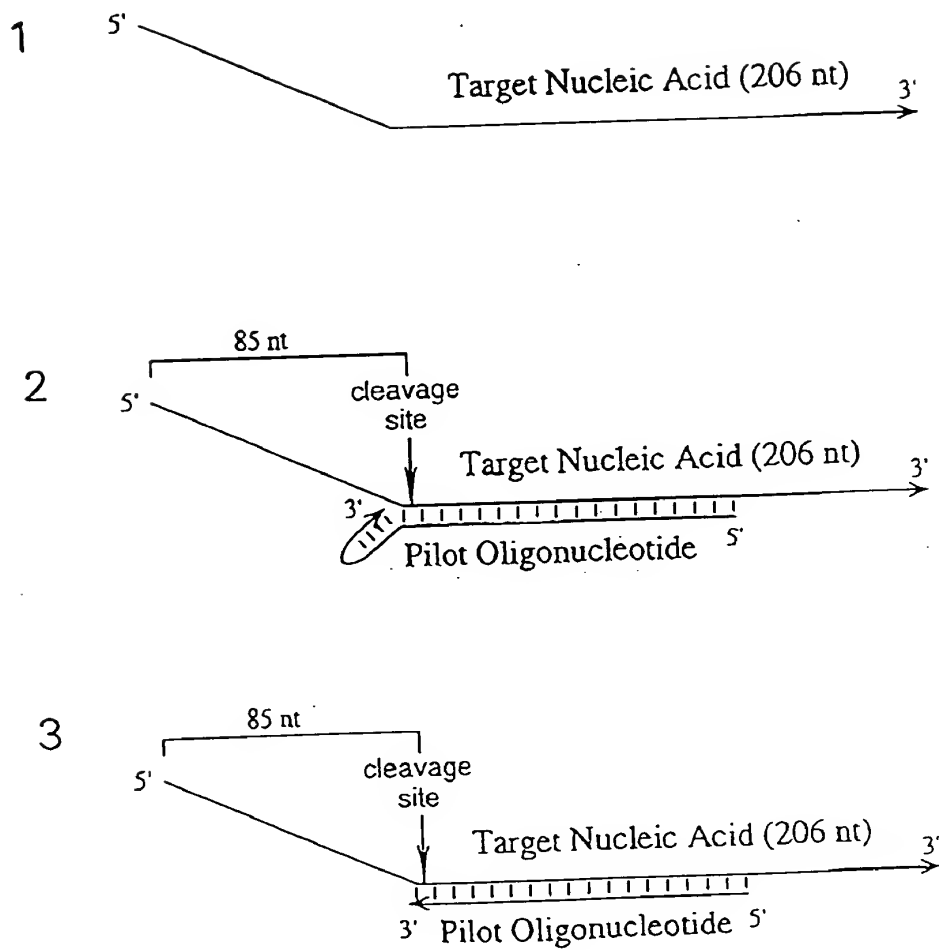


FIGURE 22B

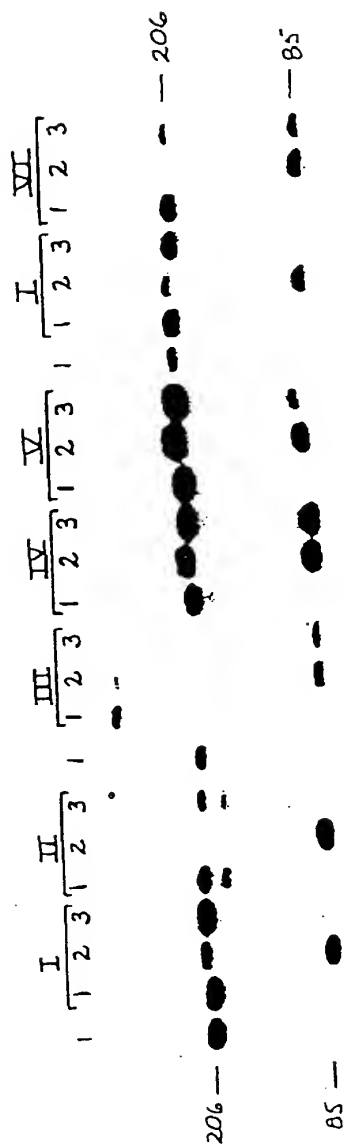


FIGURE 23

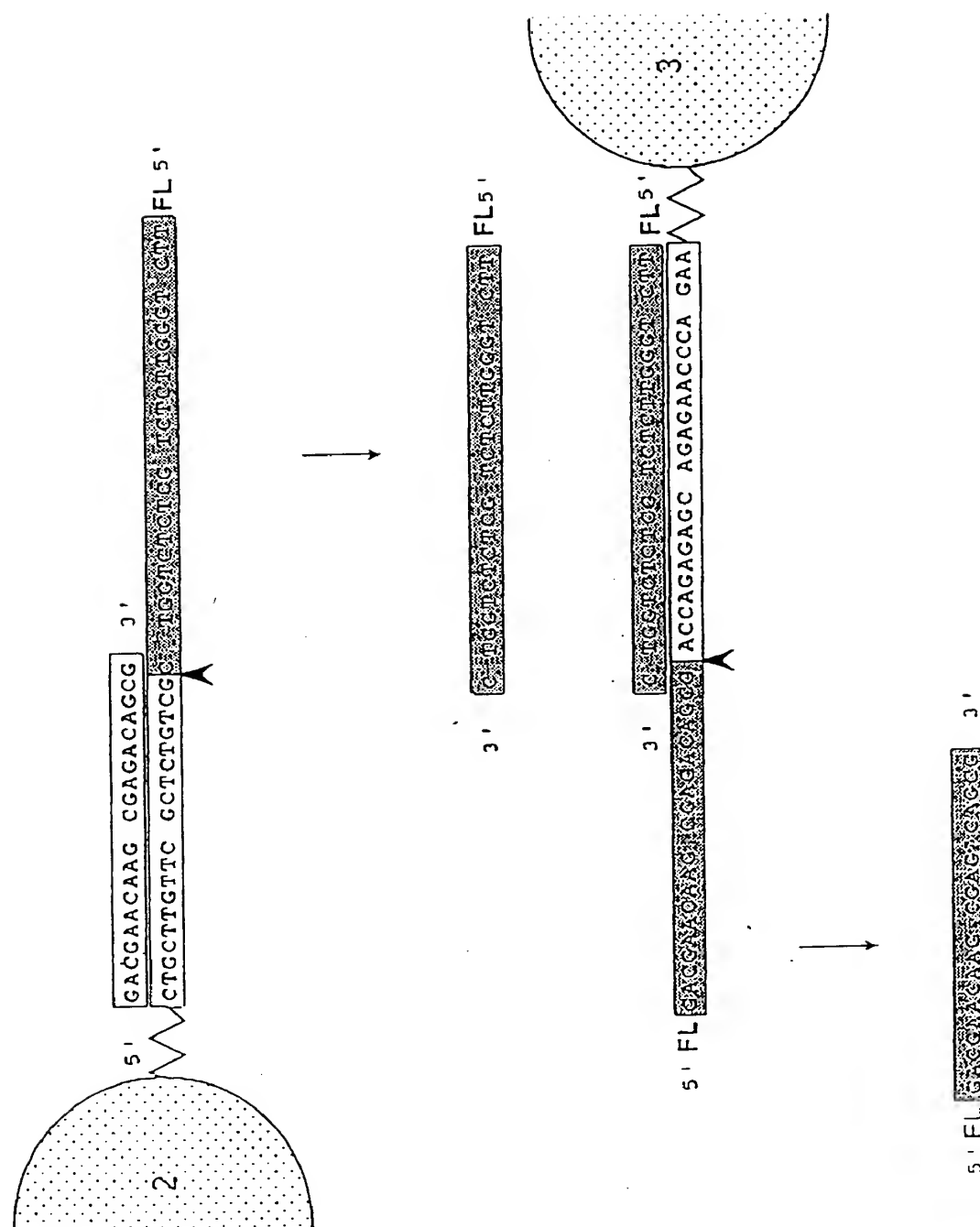


FIGURE 25

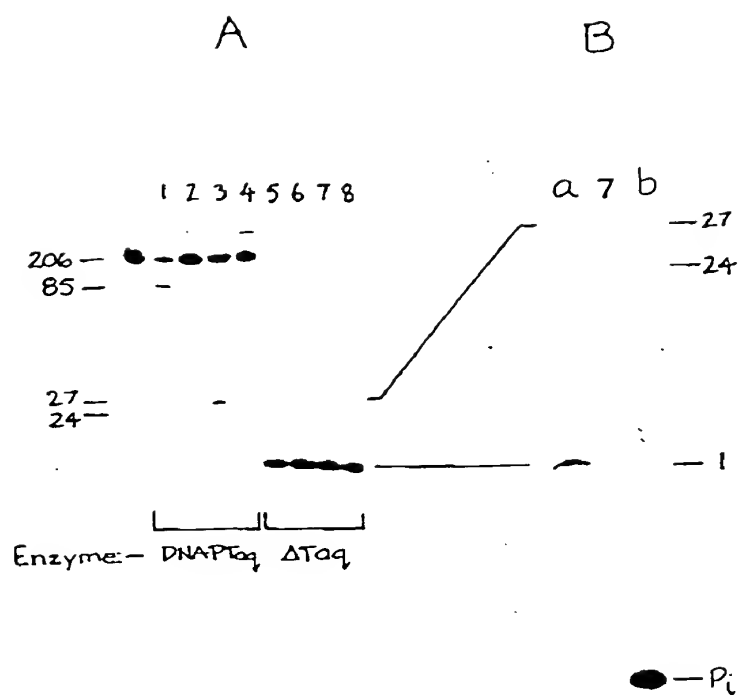
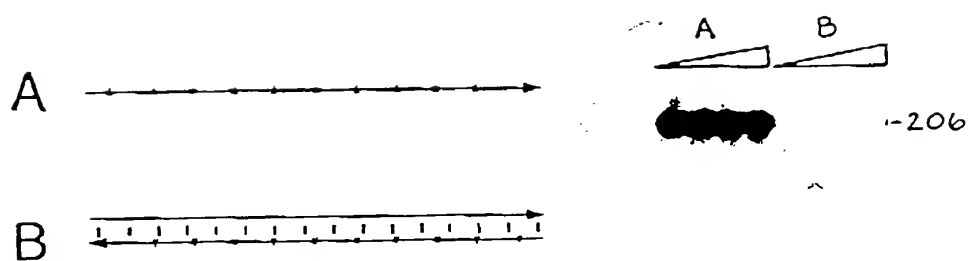


FIGURE 26



$\cdot = {}^{32}\text{P}$

FIGURE 27

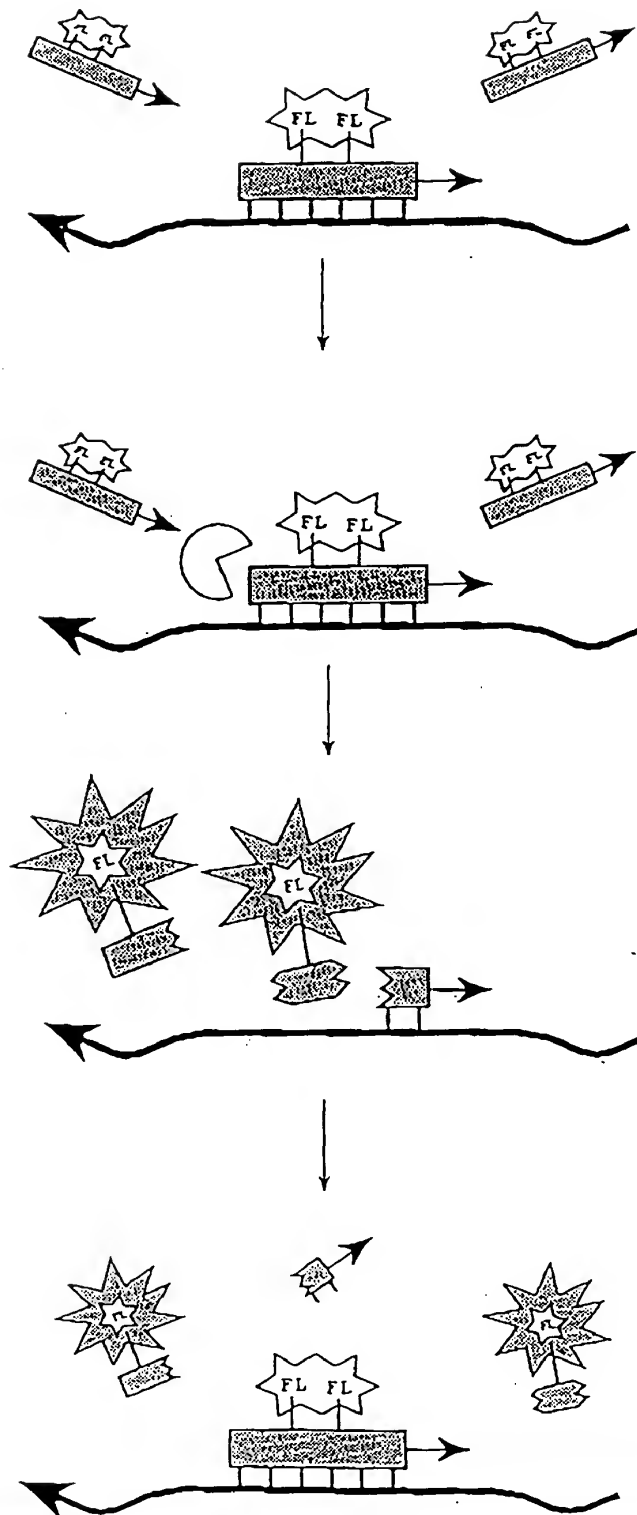
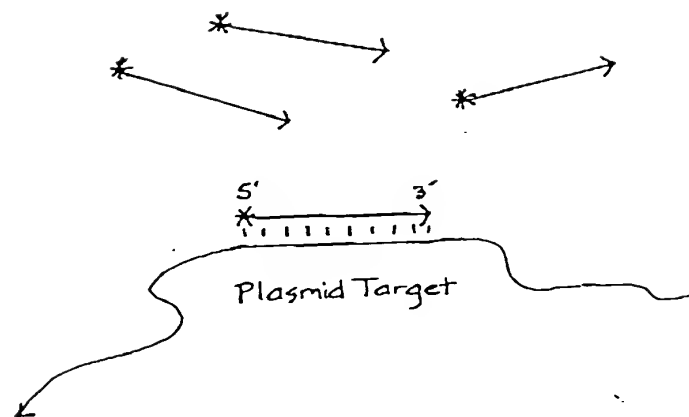


FIGURE 28A



* = ^{32}P 5' terminal phosphate

FIGURE 28B

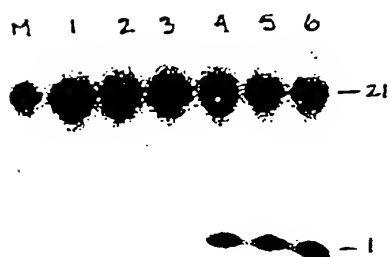


FIGURE 29

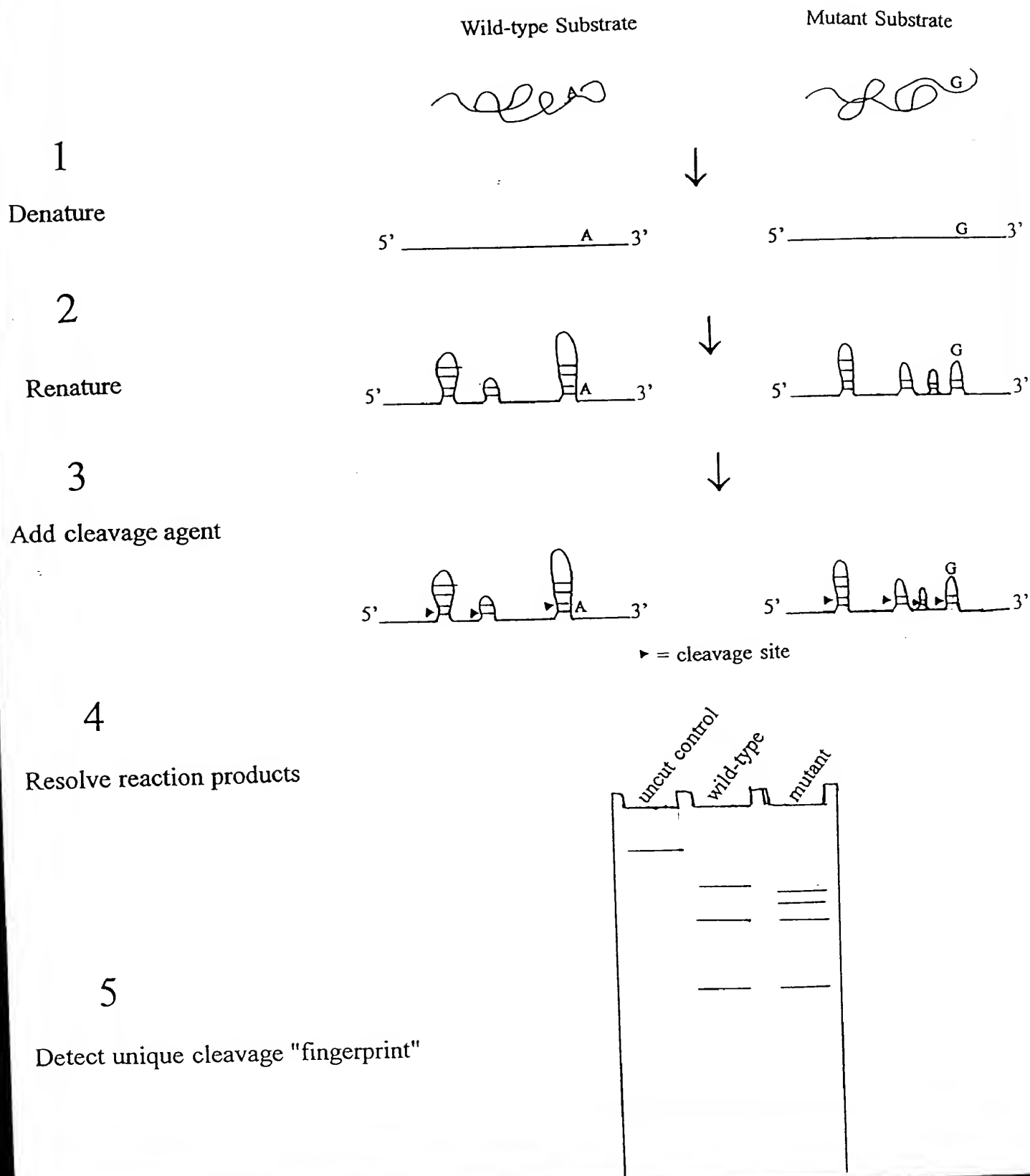


FIGURE 30

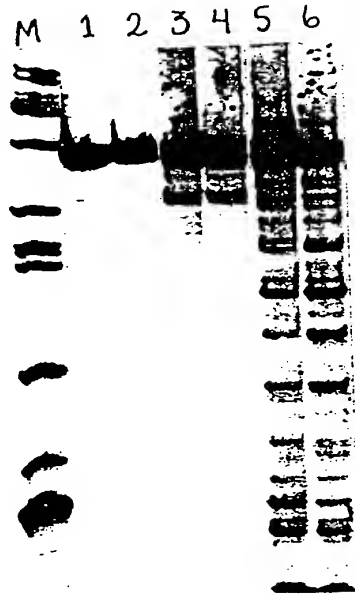


FIGURE 31

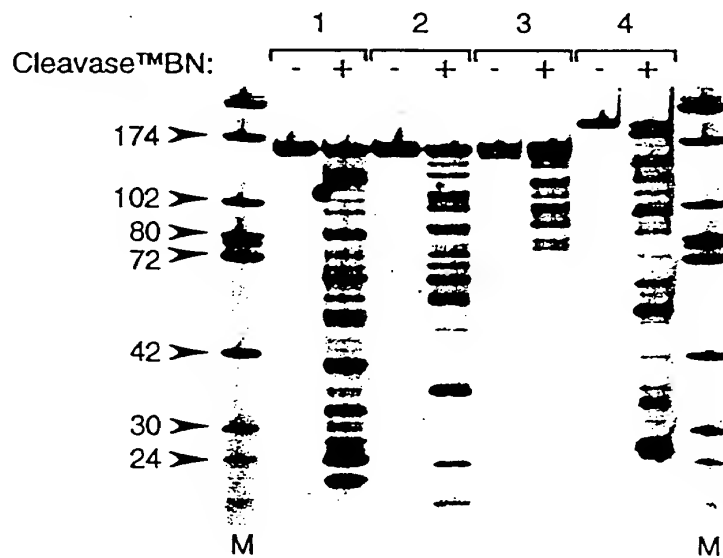


FIGURE 32

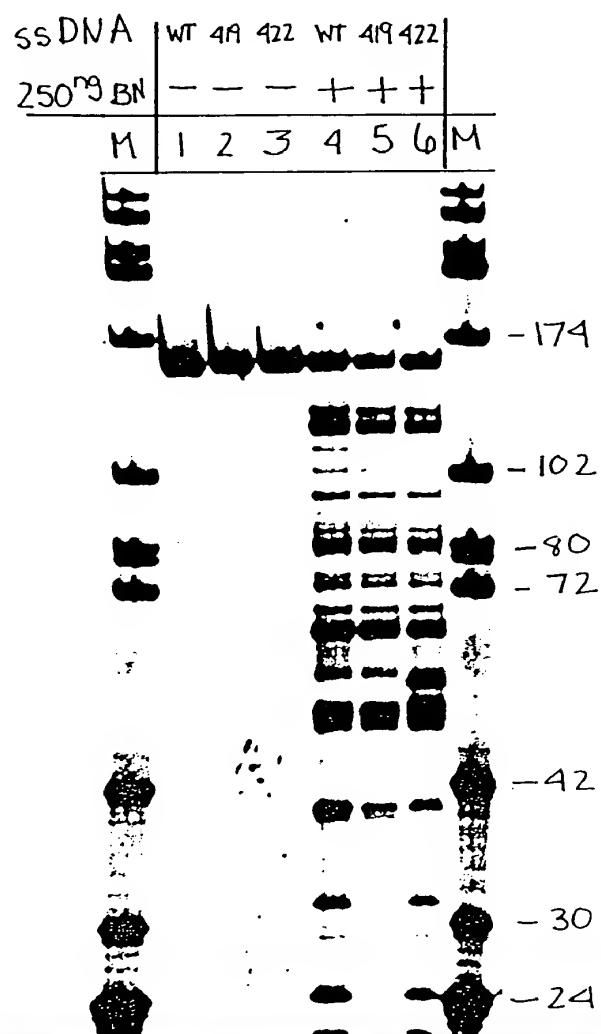


FIGURE 33

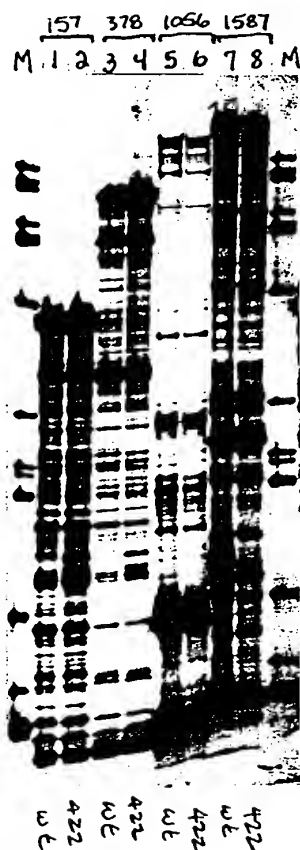


FIGURE 34

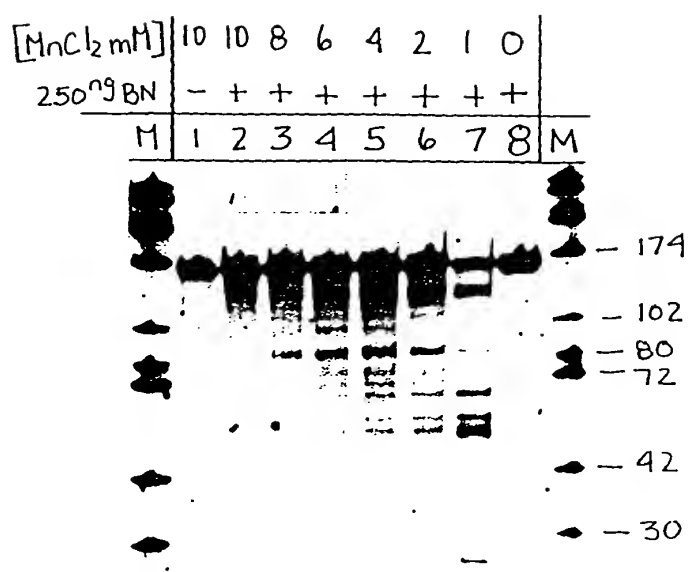


FIGURE 35

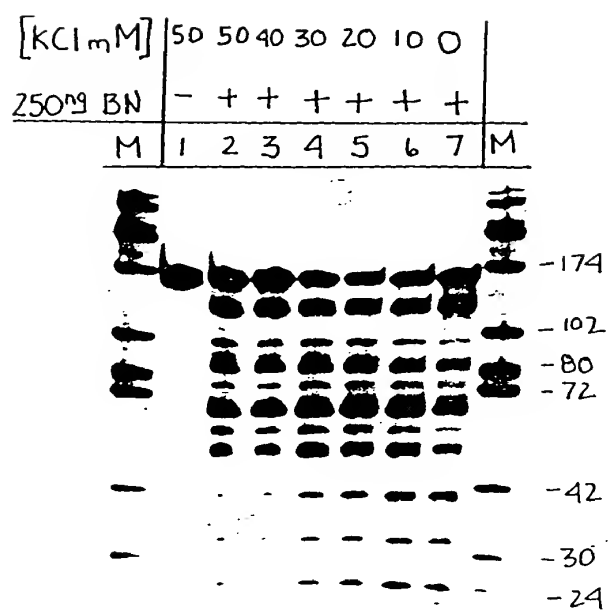


FIGURE 36

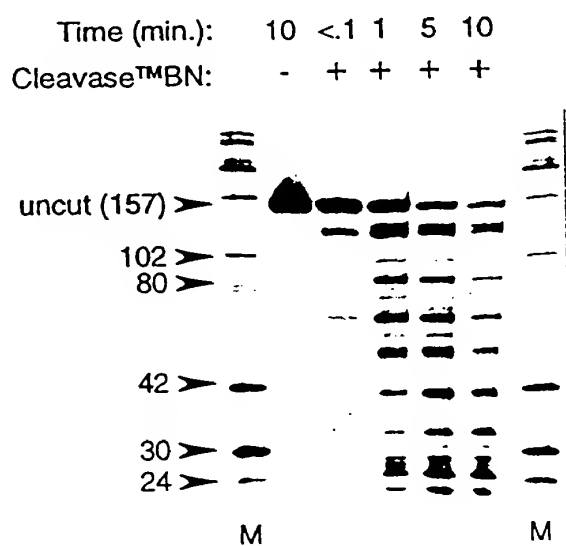


FIGURE 37

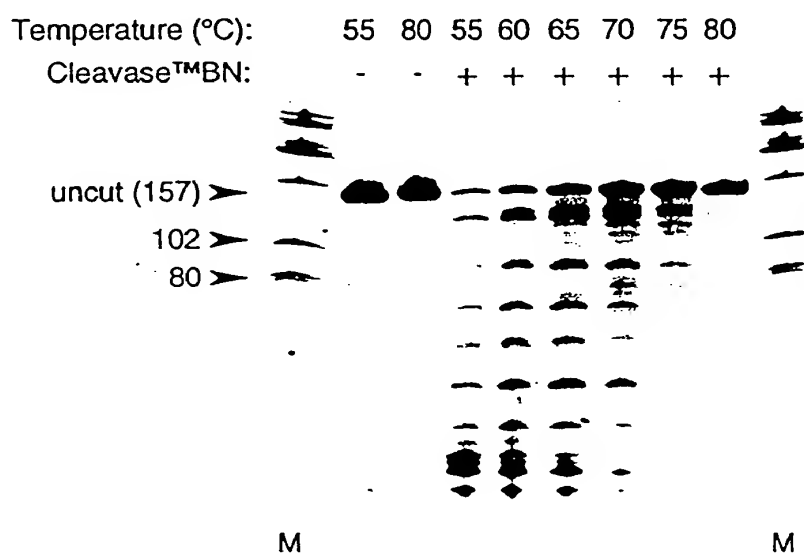


FIGURE 39

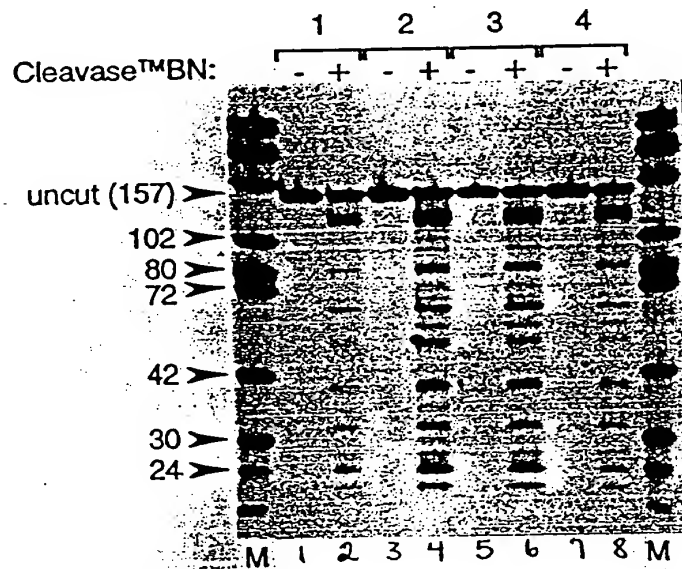


FIGURE 40

strand	5'-BIOTIN SENSE STRAND						5'-FLUORESCCEIN ANTI-SENSE strand					
	ss DNA						ss DNA					
	WT	419	422	WT	419	422	WT	419	422	WT	419	422
250 ^{ng} BN	-	-	-	+	+	+	+	+	+	-	-	-
M	1	2	3	4	5	6	7	8	9	10	11	12

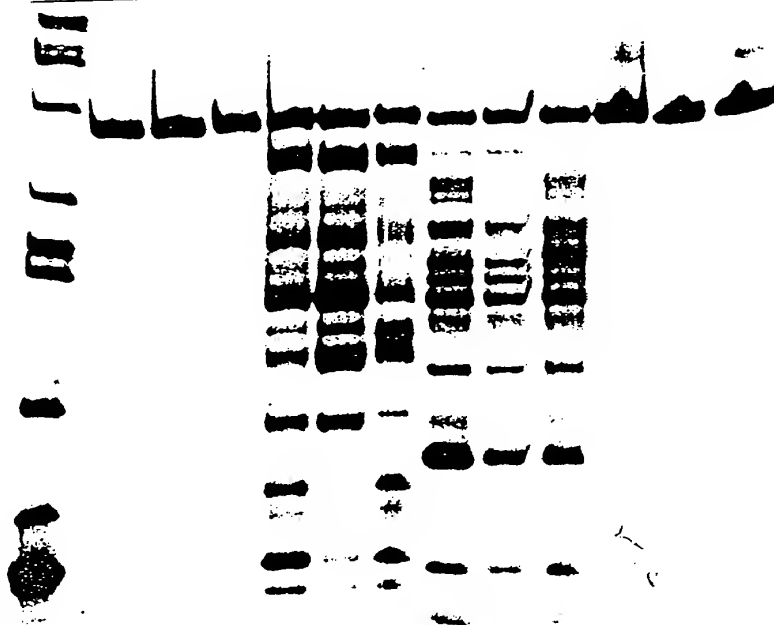


FIGURE 41

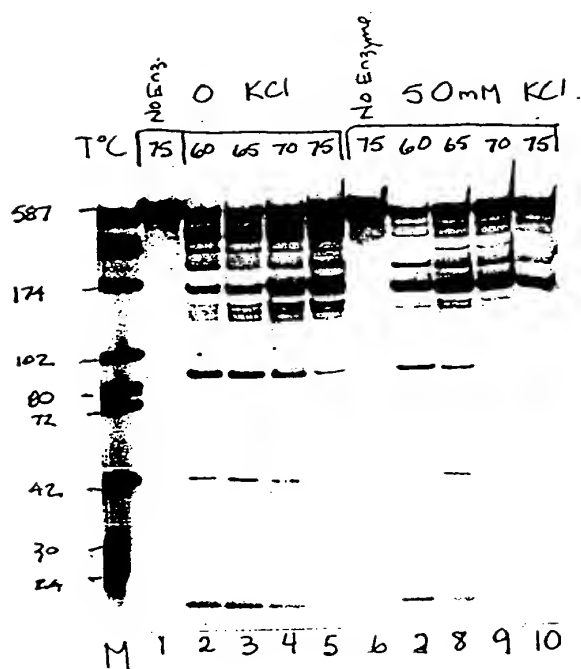


FIGURE 42

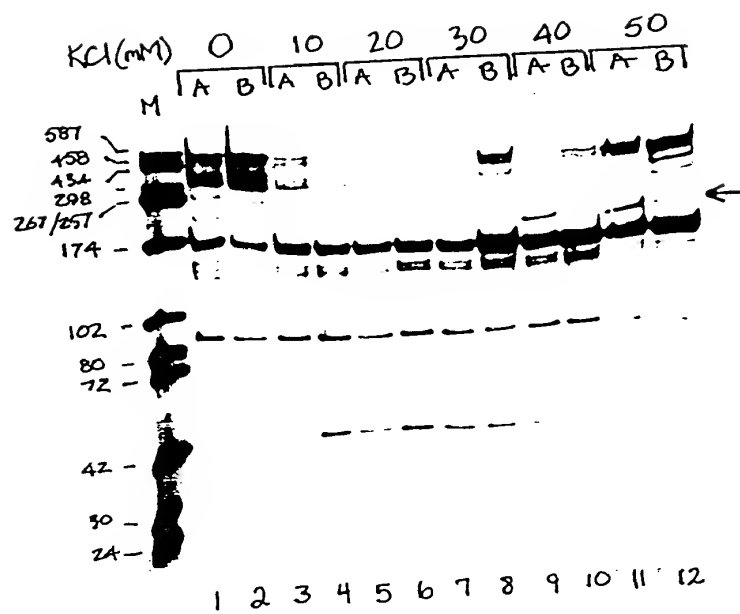


FIGURE 43



FIGURE 44

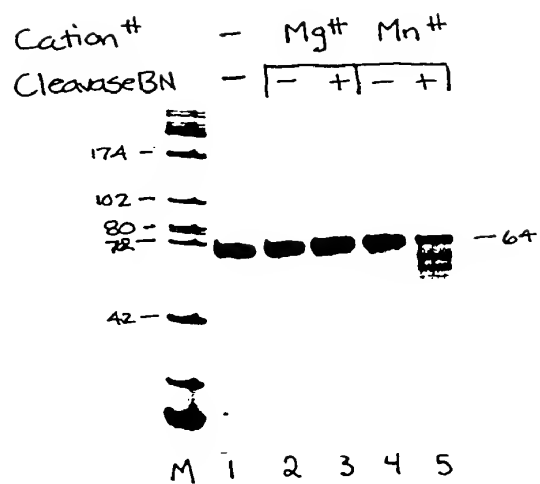


FIGURE 45

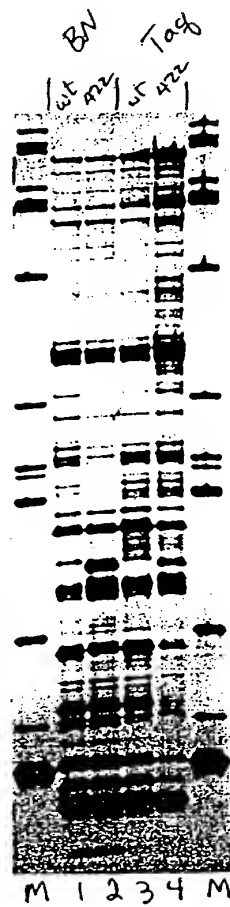


FIGURE 46

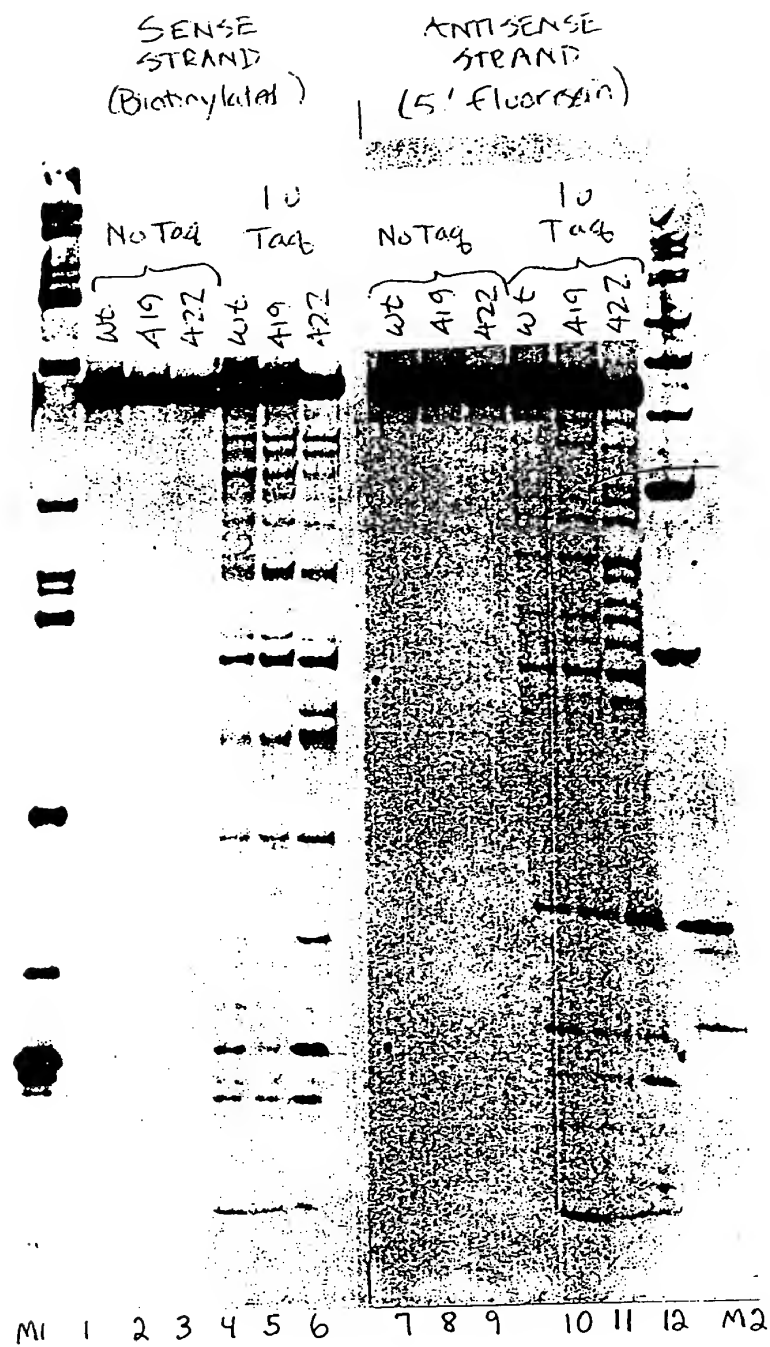
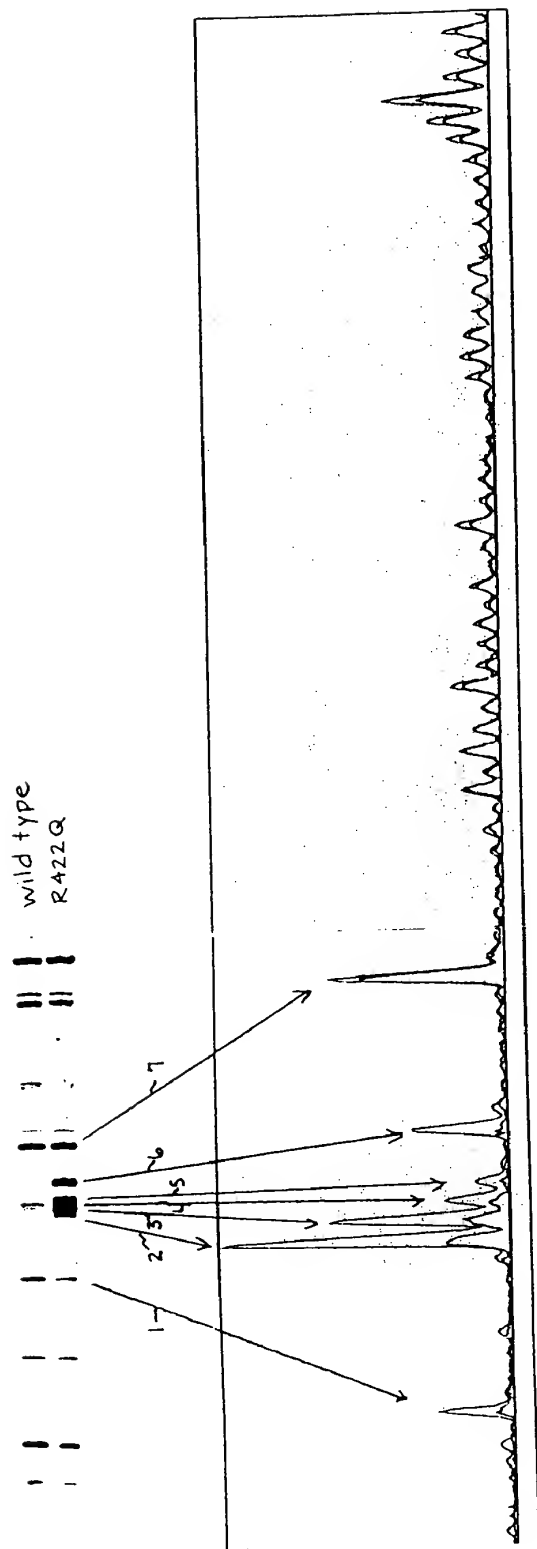


FIGURE 47



FIGURE 48



08/520946

FIGURE 49

L. 100. 8-1 5'GGCTGACAAGGAAGAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG ATGTTACGGGAGGTACTGGGAGGAGCCGGTCGGGAACGCCACTCTCT
 (SEQ ID NO: 76) 3'CCGACTGTTCTTCCCTTTAGCGACTCTGTGTCCTGAAAGGTGTTCCCC TACAATGCCCTCCATGACCCCTCTCGGCCAGCCCTTGGGGTGAGAGA
 L. 46. 16-10 5'GGCTGACAAGGAAGAACTCGCTGAGATAGCAGGACTTTCCACAAGGGG ATGTTATGGGGAGG-----AGCCGGTCGGGAACACCCACTTTCT
 (SEQ ID NO: 77) 3'CCGACTGTTCTTCCCTTTAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC TACAATACCCCTCC-----TCGGCCAGCCCTTGTGGGTGAAAGA
 L. 46. 16-12 5'GGCTGACAAGGAAGAACTCGCTGAGATAGCAGGACTTTCCACAAGGGG ATGTTATGGGGAGG-----AGCCGGTCGGGAACACCCACTTTCT
 (SEQ ID NO: 78) 3'CCGACTGTTCTTCCCTTTAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC TACAATACCCCTCC-----TCGGCCAGCCCTTGTGGGTGAAAGA
 L. 19. 16-3 5'GGCTGACAAGGAAGAACTCGCTGAGACAGCAGGACTTTCCACAAGGGG ATGTTACGGGGAGGTACTGGGAGGAGCCGGTCGGGAACGCCCTCTCT
 (SEQ ID NO: 79) 3'CCGACTGTTCTTCCCTTTAGCGACTCTGTCGTCCTGAAAGGTGTTCCCC TACAATGCCCTCCATGACCCCTCTCTCGGCCAGCCCTTGGGGGGAGAGA
 L. CEM/251 5'GGCTGACAAGGAAGAACTCGCTGAAACAGCAGGACTTTCCACAAGGGG ATGTTACGGGGAGGTACTGGGAAGGAGCCGGTCGGGAACGCCCTTTCT
 (SEQ ID NO: 80) 3'CCGACTGTTCTTCCCTTTAGCGACTTTGTCGTCCTGAAAGGTGTTCCCC TACAATGCCCTCCATGACCCCTTTCTCGGCCAGCCCTTGGGGGTGAAAGA
 L. 36. 8-3 5'GGCTGACAAGGAAGAACTCGCTGAGACAGCAGGACTTTCCACAAGGGG ATGTTACGGGGAGGTACTGGGAGGAGCCGGTCGGGAACGCCCTCTCT
 (SEQ ID NO: 81) 3'CCGACTGTTCTTCCCTTTAGCGACTCTGTCGTCCTGAAAGGTGTTCCCC TACAATGCCCTCTCCATGACCCCTCTCTCGGCCAGCCCTTGGGGGTGAAAGA
 L. 100. 8-1 5'TGATGTATAAATATCACTGCATTTCCGCTCTGTATTGATCGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
 3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCT CTCCGACCGTCTAACTCGGACCCCTCCAGAGAGGTCGTGATCGTCCATC
 L. 46. 16-10 5'TGATGTATAAATATCACTGCATTTCCGCTCTGTATTGATCGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
 3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCT CTCCGACCGTCTAACTCGGACCCCTCCAGAGAGGTCGTGATCGTCCATC
 L. 46. 16-12 5'TGGTGTATAAATATCACTGCATTTCCGCTCTGTATTGATCGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
 3'ACCACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCT CTCCGACCGTCTAACTCGGACCCCTCCAGAGAGGTCGTGATCGTCCATC
 L. 19. 16-3 5'TGATGTATAAATATCACTGCATTTCCGCTCTGTATTGATCGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
 3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCT CTCCGACCGTCTAACTCGGACCCCTCCAGAGAGGTCGTGATCGTCCATC
 L. CEM/251 5'TGATGTATAAATATCACTGCATTTCCGCTCTGTATTGATCGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
 3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCT CTCCGACCGTCTAACTCGGACCCCTCCAGAGAGGTCGTGATCGTCCATC
 L. 36. 8-3 5'TGATGTATAAATATCACTGCATTTCCGCTCTGTATTGATCGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTAGGAGGTTCTCTCCAGCACTAGCAGGTAG
 3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCT CTCCGACCGTCTAACTCGGACCCCTCCAGAGAGGTCGTGATCGTCCATC

300

250

L. 100.8-1 5' AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACTTG3CCGGTGCTGGG CAGAGTGGCTCCACGCTTGCTTTAAAGACCTCTTCAATAAAGCTGCC
(Seq ID NO: 76) 3' TCGGACCCACAAGGACGATCTGAGAGTGGTCTGTAACCGGCCACGACCC GTCTCACCGAGGTGCGAACGAACTTCTGGAGAGTTATTTTCGACGG

L. 46.16-10 5' AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACTTAGCCAGTGCTGGG CAGAGTGGCTCCACGCTTGCTTTAAAGACCTCTTCAATAAAGCTGCC
(Seq ID NO: 77) 3' TCGGACCCACAAGGACGATCTGAGAGTGGTCTGTAATCGGTACGACCC GTCTCACCGAGGTGCGAACGAACTTCTGGAGAGTTATTTTCGACGG

L. 46.16-12 5' AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACTTGCCAGTGCTGGG CAGAGTGGCTCCACGCTTGCTTTAAAGACCTCTTCAATAAAGCTGCC
(Seq ID NO: 78) 3' TCGGACCCACAAGGACGATCTGAGAGTGGTCTGTAACCGGTACGACCC GTCTCACCGAGGTGCGAACGAACTTCTGGAGAGTTATTTTCGACGG

L. 19.16-3 5' AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACTTGCCGGTGCTGGG CAGAGTGGCTCCACGCTTGCTTTAAAGACCTCTTCAATAAAGCTGCC
(Seq ID NO: 79) 3' TCGGACCCACAAGGACGATCTGAGAGTGGTCTGTAACCGGCCACGACCC GTCTCACCGAGGTGCGAACGAACTTCTGGAGAGTTATTTTCGACGG

L. CEM/251 5' AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACTTGCCGGTGCTGGG CAGAGTGGCTCCACGCTTGCTTTAAAGACCTCTTCAATAAAGCTGCC
(Seq ID NO: 80) 3' TCGGACCCACAAGGACGATCTGAGAGTGGTCTGTAACCGGCCACGACCC GTCTCACCGAGGTGCGAACGAACTTCTGGAGAGTTATTTTCGACGG

L. 36.8-3 5' AGCCTGAGTGTTCCCTGCTAACTCTCACCAGCACTTGCCGGTGCTGGG CAGAGCGGCTCCACGCTTGCTTTGCTTTAAAGACCTCTTCAATAAAGCTGCC
(Seq ID NO: 81) 3' TCGGACTCACAAAGGACGATTTGAGAGTGGTCTGTAACCGGCCACGACCC GTCTCGCCGAGGTGCGAACGAACTTCTGGAGAGTTATTTTCGACGG

350

L. 100.8-1 5' ATTTTAGAAGTAGCCAGTGTTGCCATCTCTCCTAGCCGCCCTG G 3'
3' TAAAAATCTTCATCCGGTACACACAAGGGTAGAGAGGATCGGCGGGGAC C 5'

L. 46.16-10 5' ATTTTAGAAGTAGCCAGTGTTGCCATCTCTCCTAGCCGCCCTG G 3'
3' TAAAAATCTTCATCCGGTACACACAAGGGTAGAGAGGATCGGCGGGGAC C 5'

L. 46.16-12 5' ATTTTAGAAGTAGCCAGTGTTGCCATCTCTCCTAGCCGCCCTG G 3'
3' TAAATCTTCATCCGGTACACACAAGGGTAGAGAGGATCGGCGGGGAC C 5'

L. 19.16-3 5' ATTTTAGAAGTAGGCTAGTGTTGCCATCTCTCCTAGCCGCCCTG G 3'
3' TAAATCTTCATCCGATCACACAAGGGTAGAGAGGATCGGCGGGGAC C 5'

L. CEM/251 5' ATTTTAGAAGTAGGCTAGTGTTGCCATCTCTCCTAGCCGCCCTG G 3'
3' TAAATCTTCATCCGATCACACAAGGGTAGAGAGGATCGGCGGGGAC C 5'

L. 36.8-3 5' ATTTTAGAAGTAGGCTAGTGTTGCCATCTCTCCTAGCCGCCCTG G 3'
3' TAAATCTTCATCCGATCACACAAGGGTAGAGAGGATCGGCGGGGAC C 5'

FIGURE 50

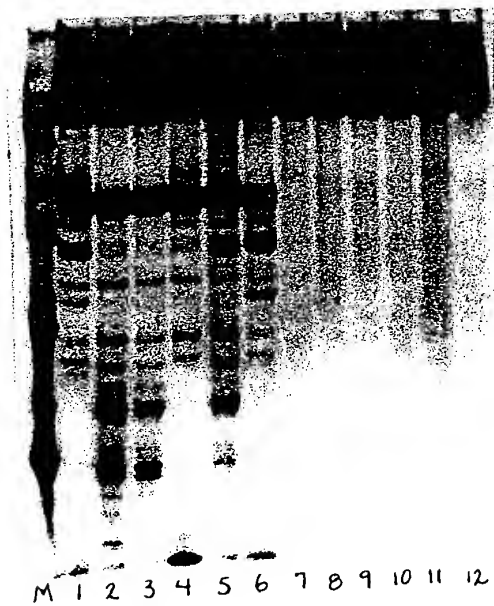


FIGURE 51

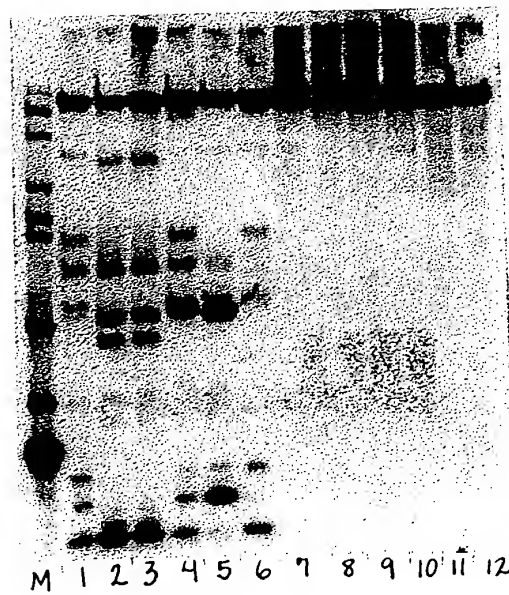


FIGURE 52

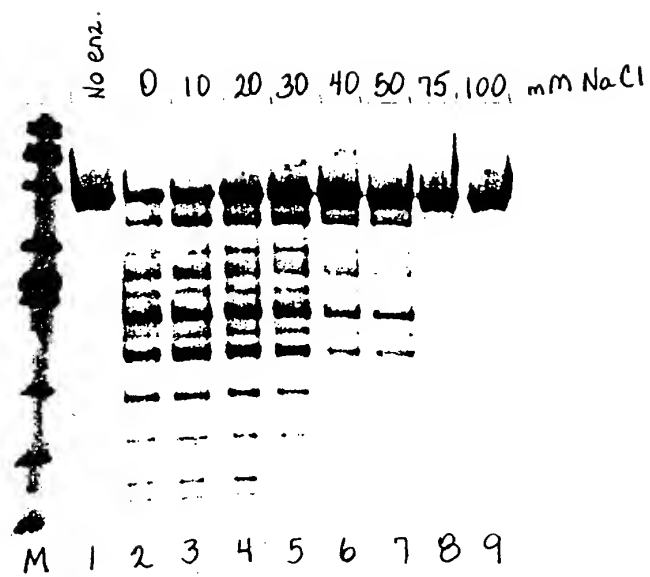


FIGURE 53

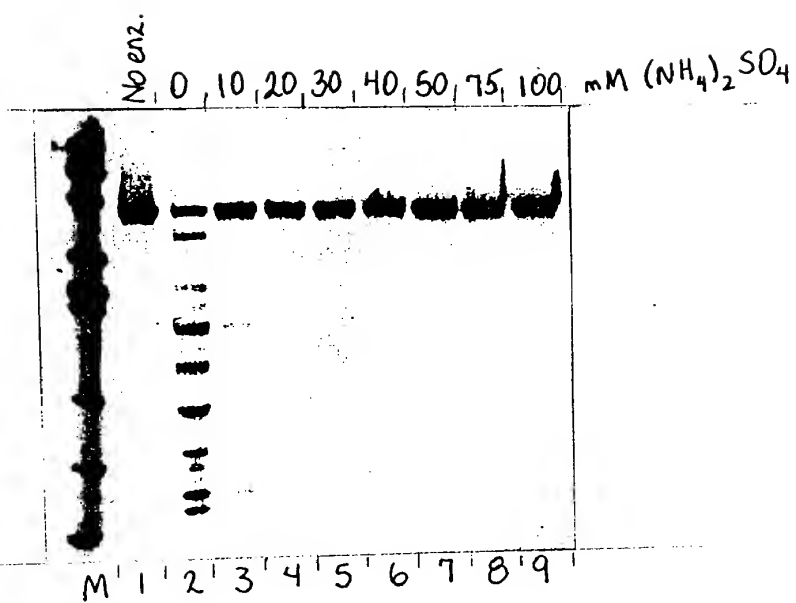


FIGURE 54

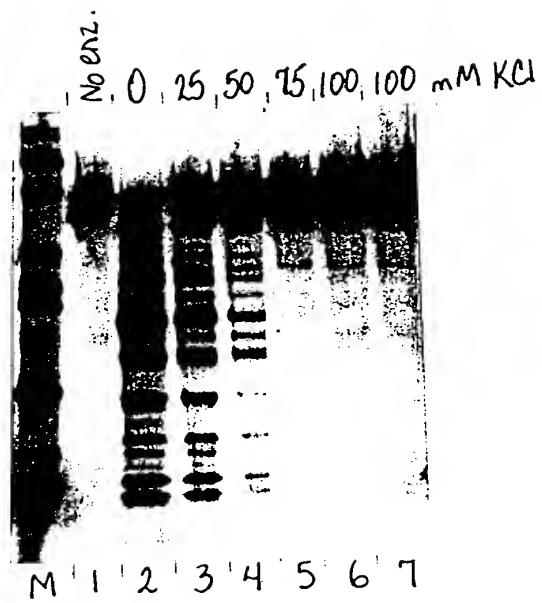


FIGURE 55

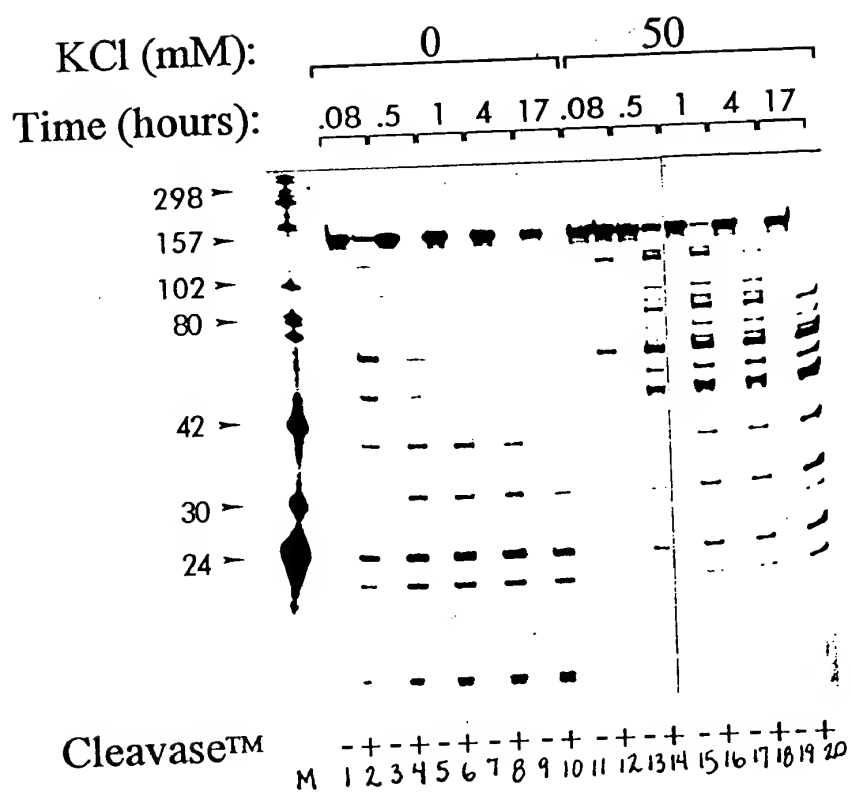


FIGURE 56

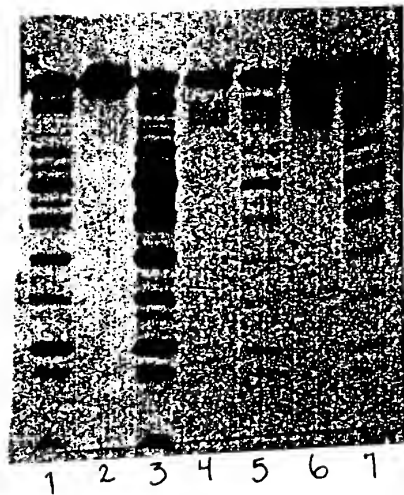


FIGURE 57

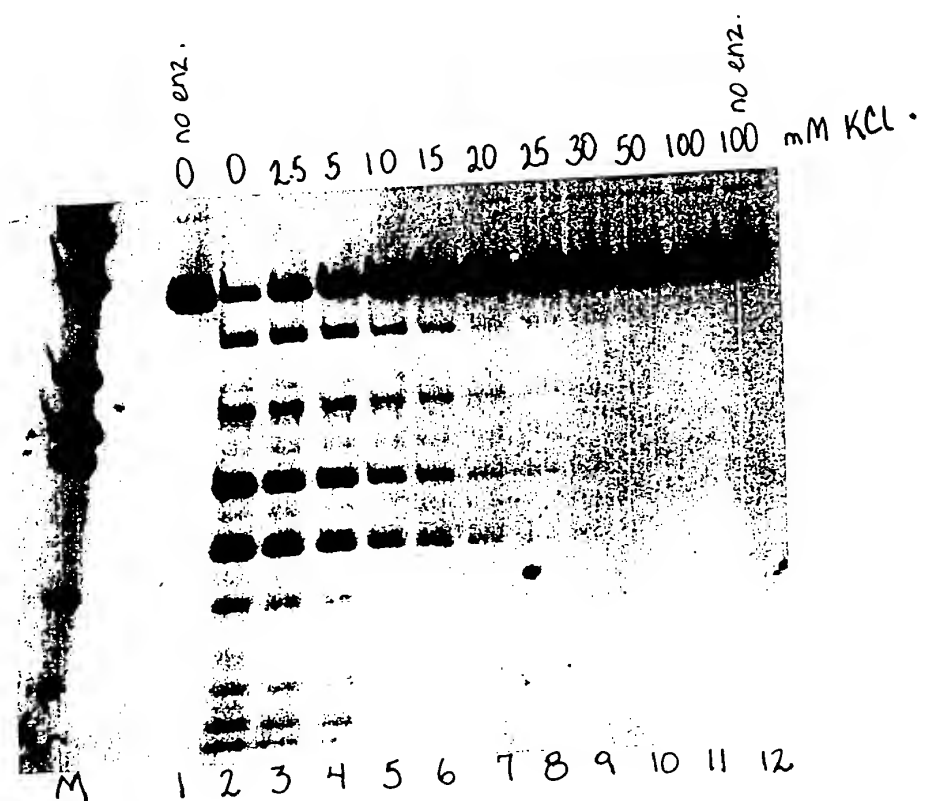


FIGURE 58

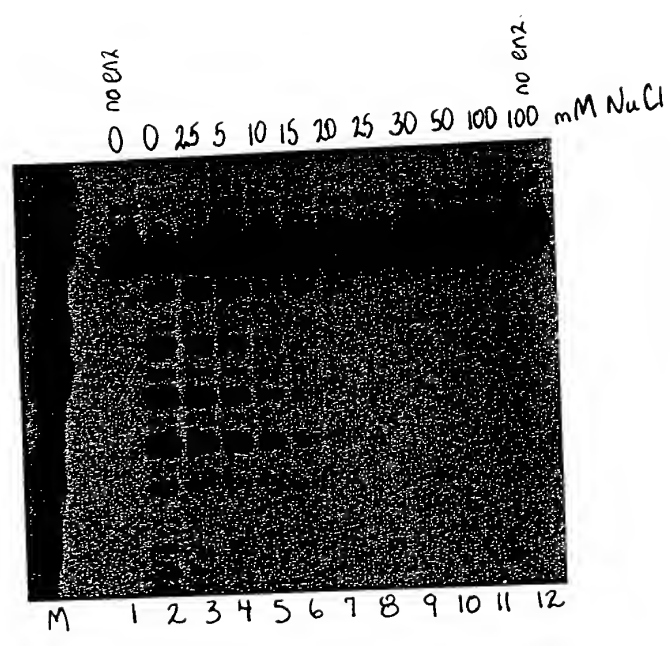


FIGURE 59

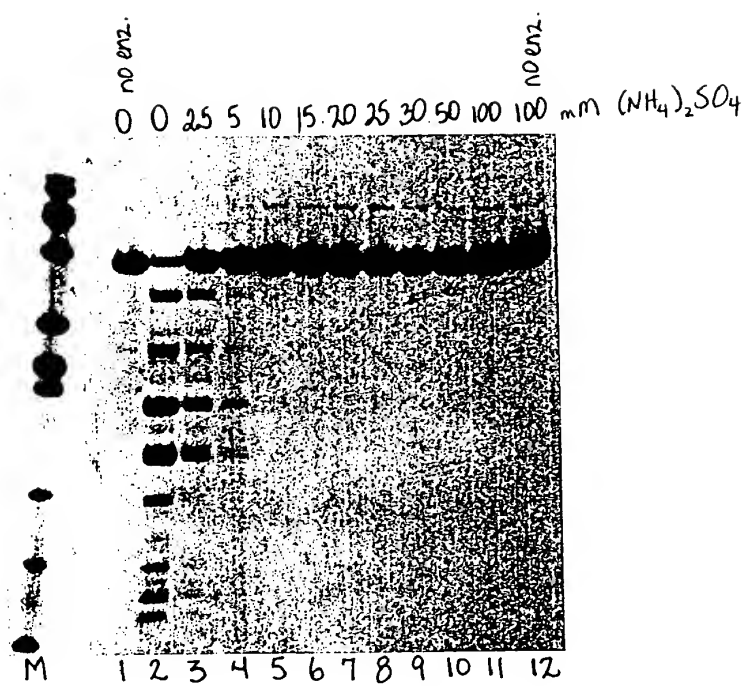


FIGURE 60

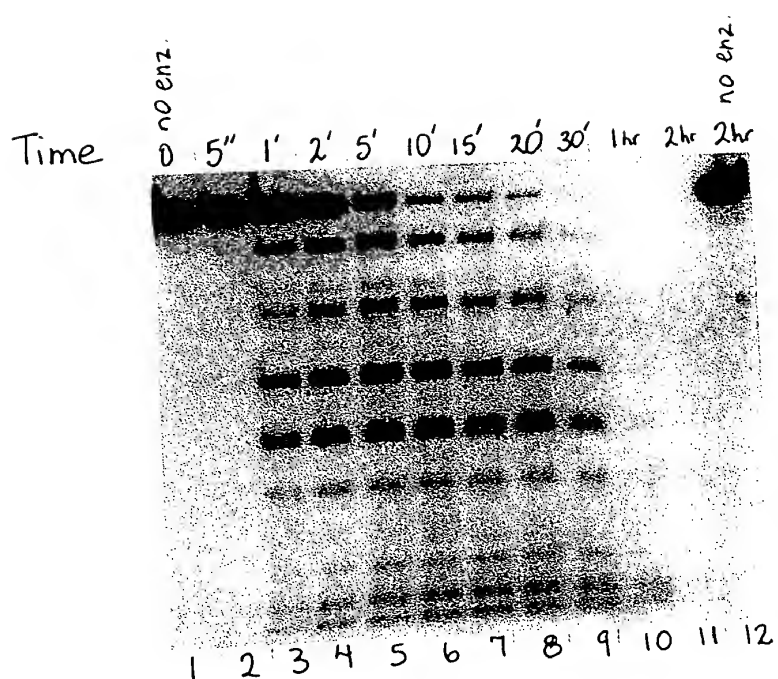


FIGURE 61

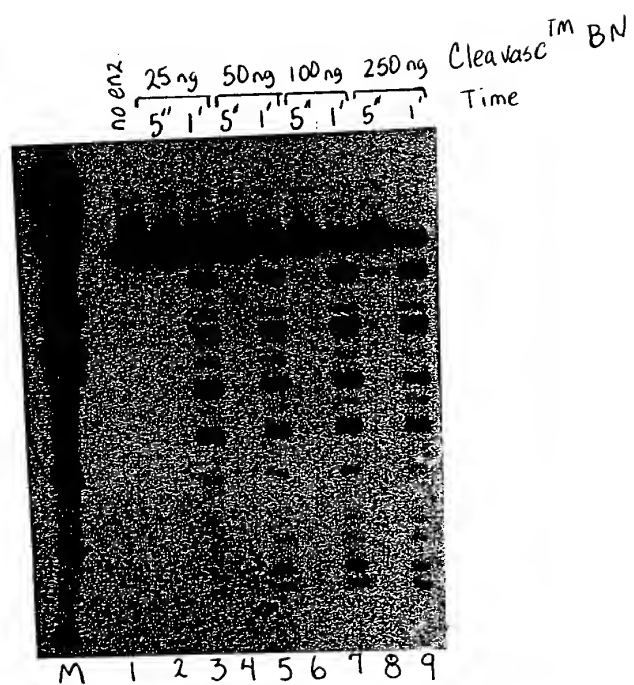


FIGURE 62

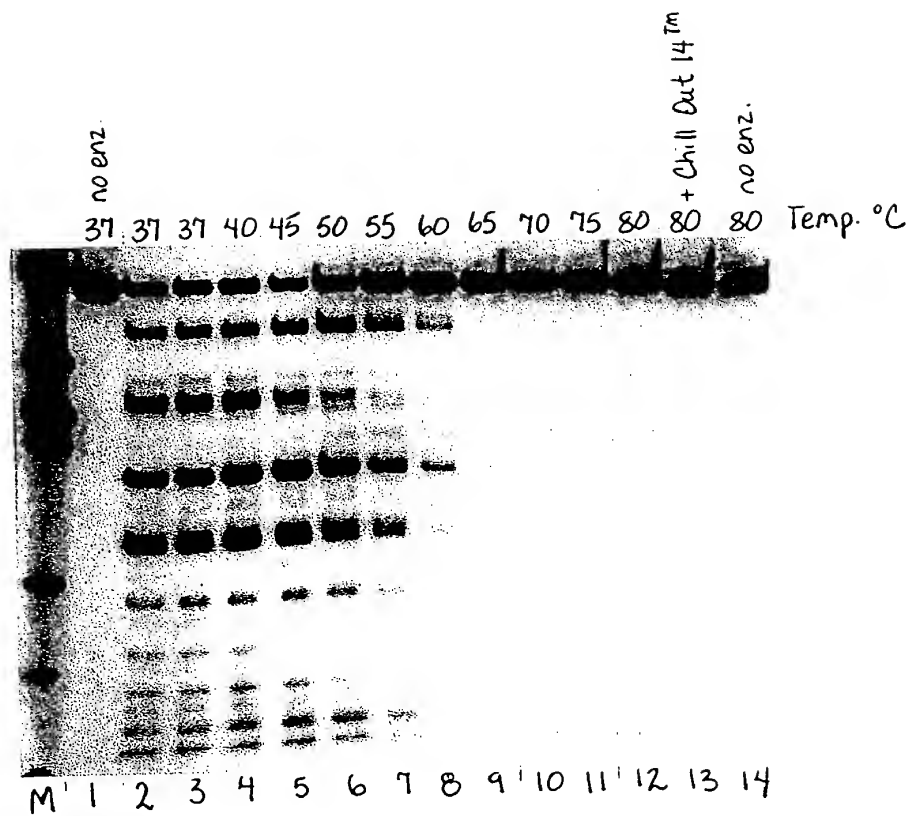


FIGURE 63

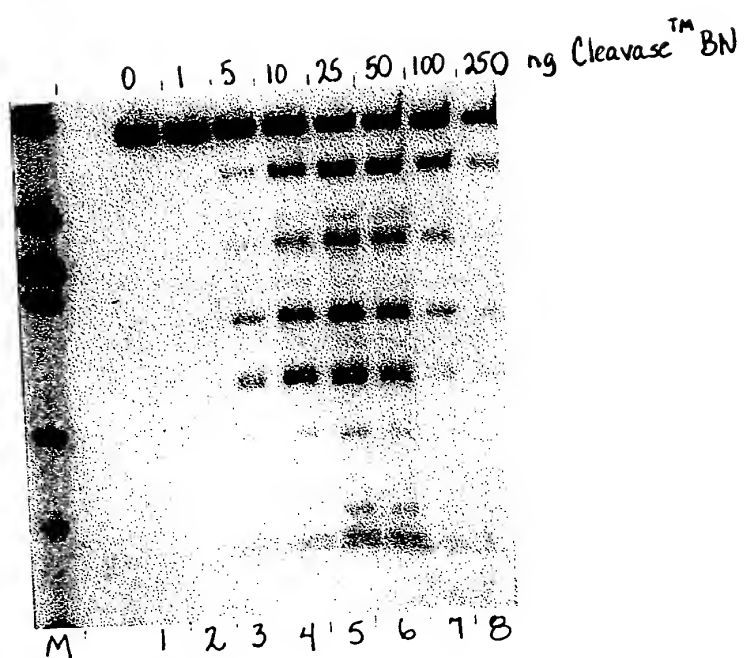
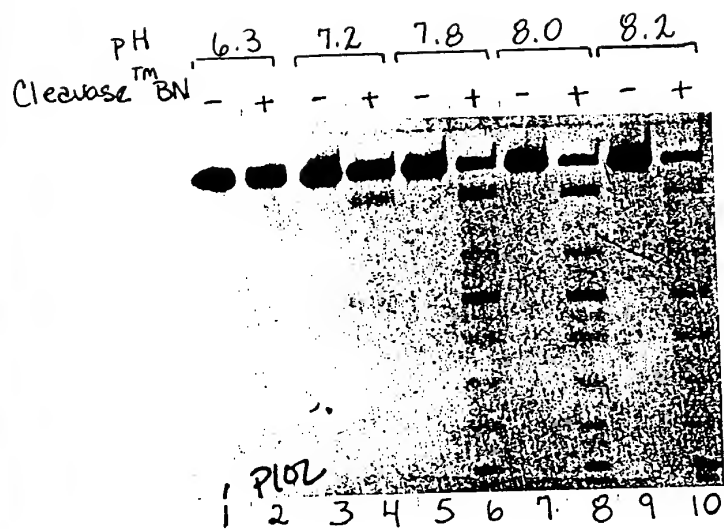


FIGURE 64

A



B

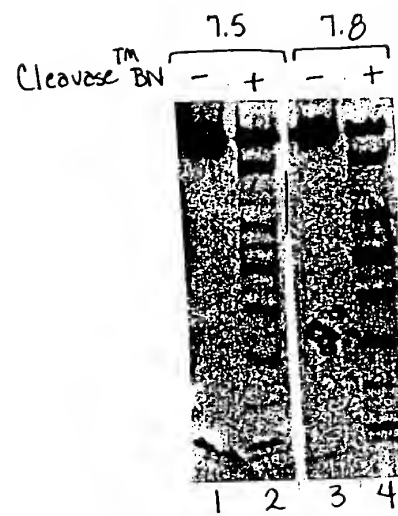
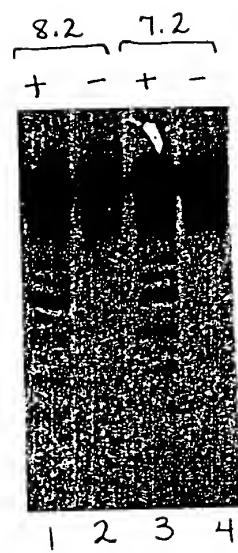


FIGURE 65

A

pH
Cleavase™ BN

B

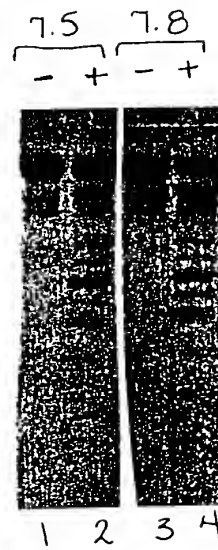


FIGURE 66

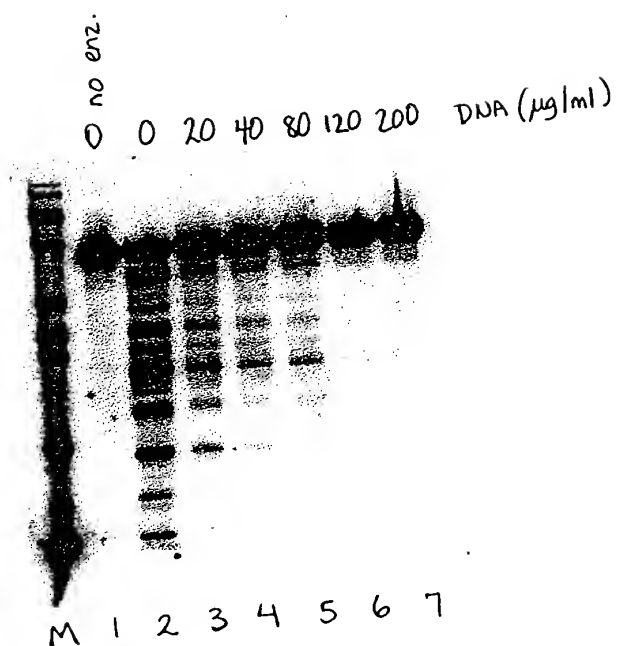


FIGURE 67

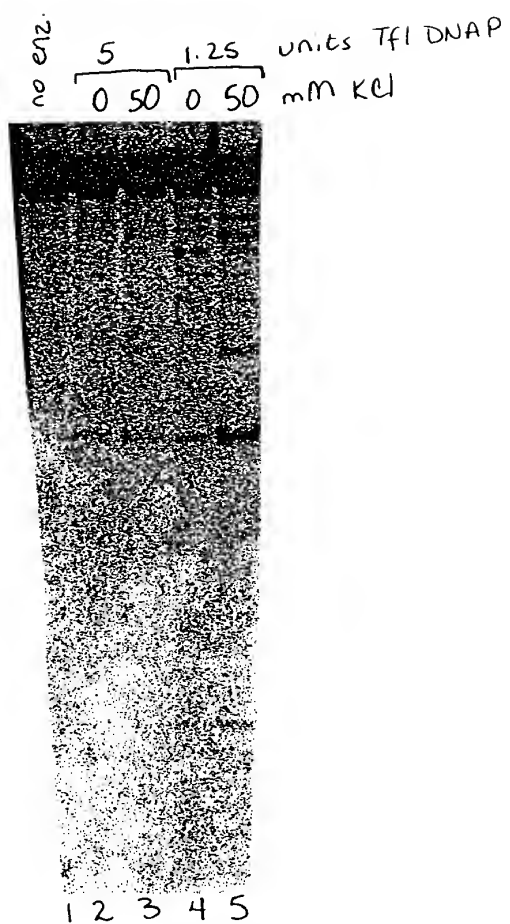


FIGURE 68

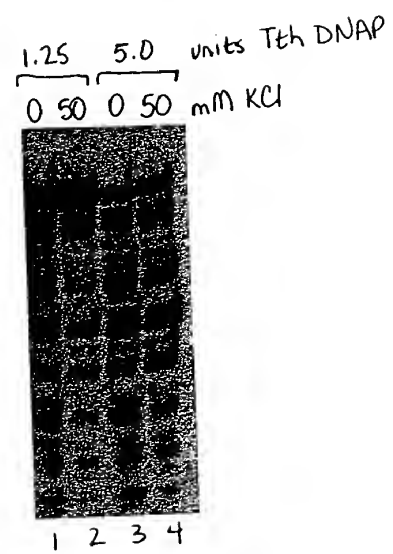


FIGURE 69

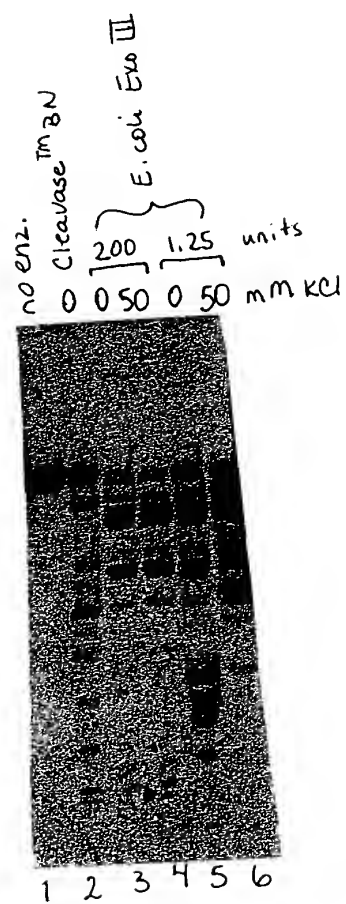


FIGURE 70

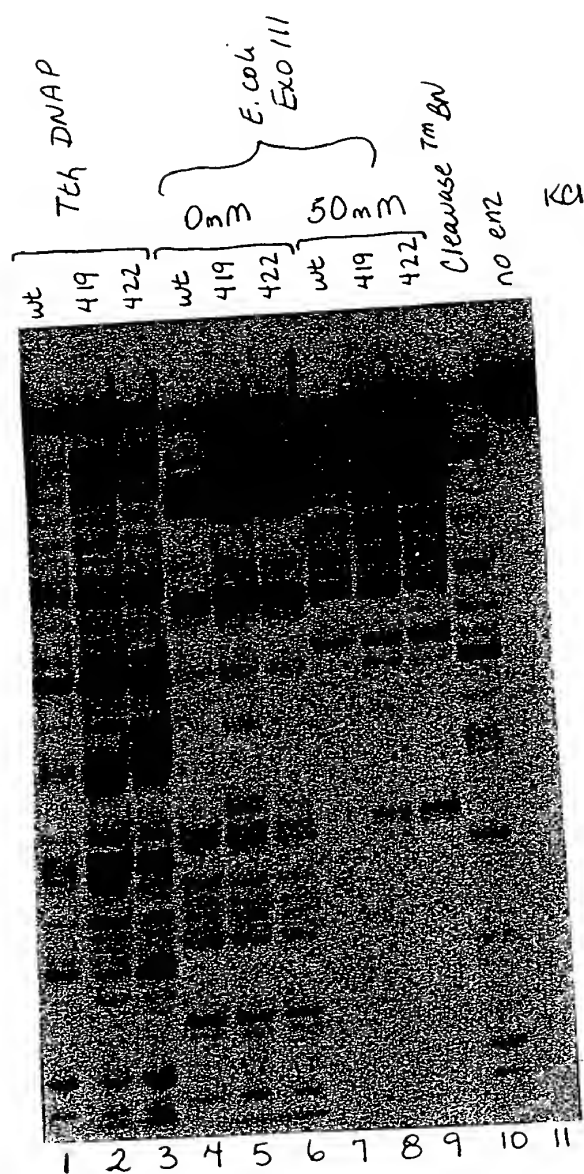


FIGURE 71

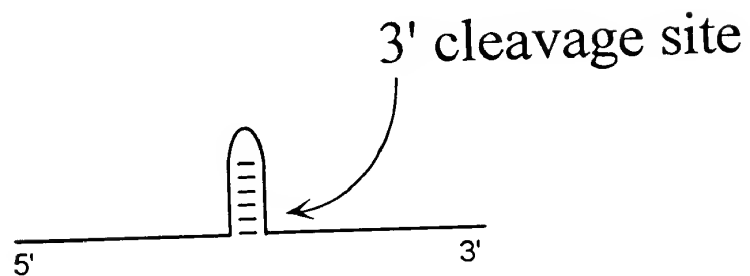
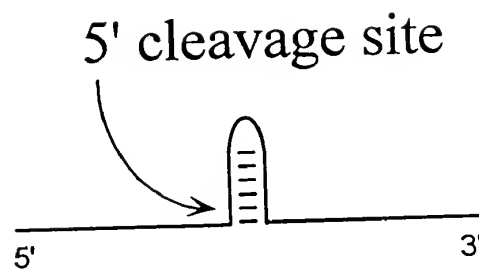
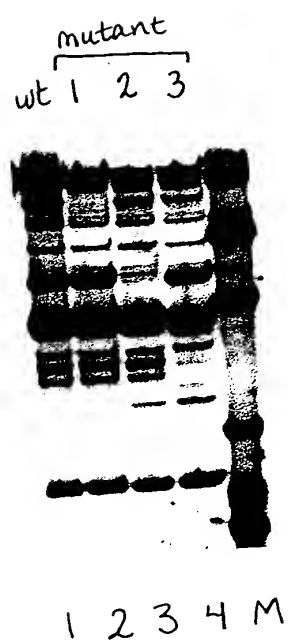


FIGURE 73



FIGURE 74

A



B

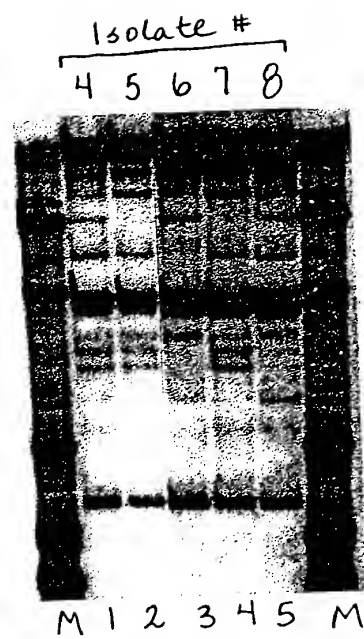


FIGURE 75

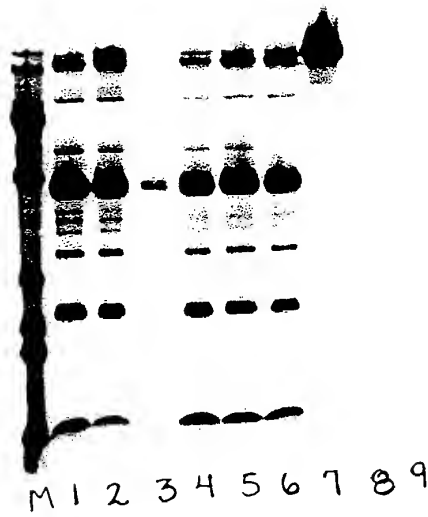


FIGURE 76

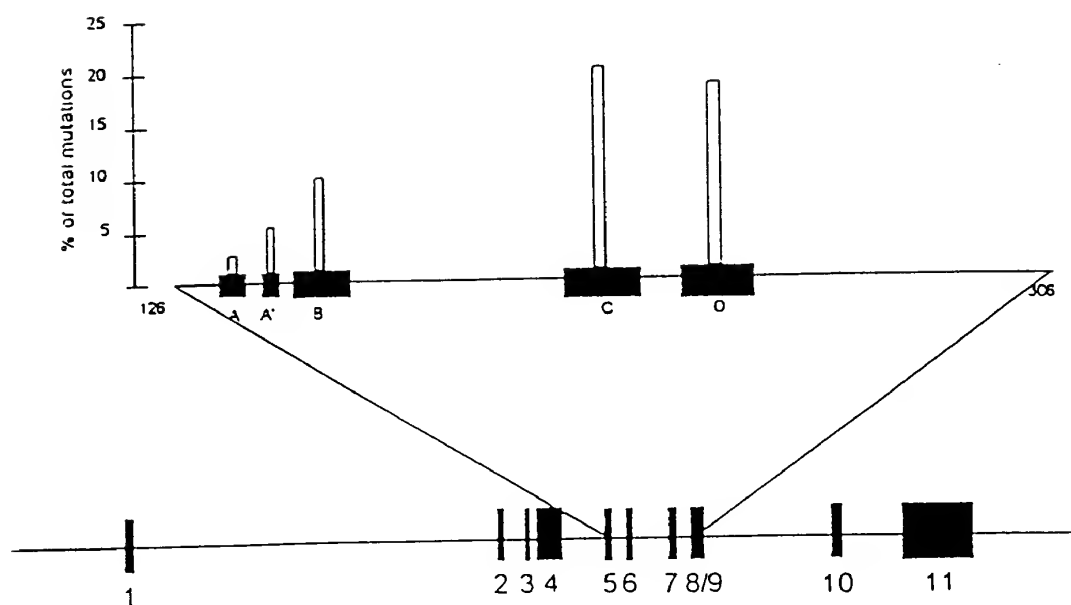


FIGURE 77

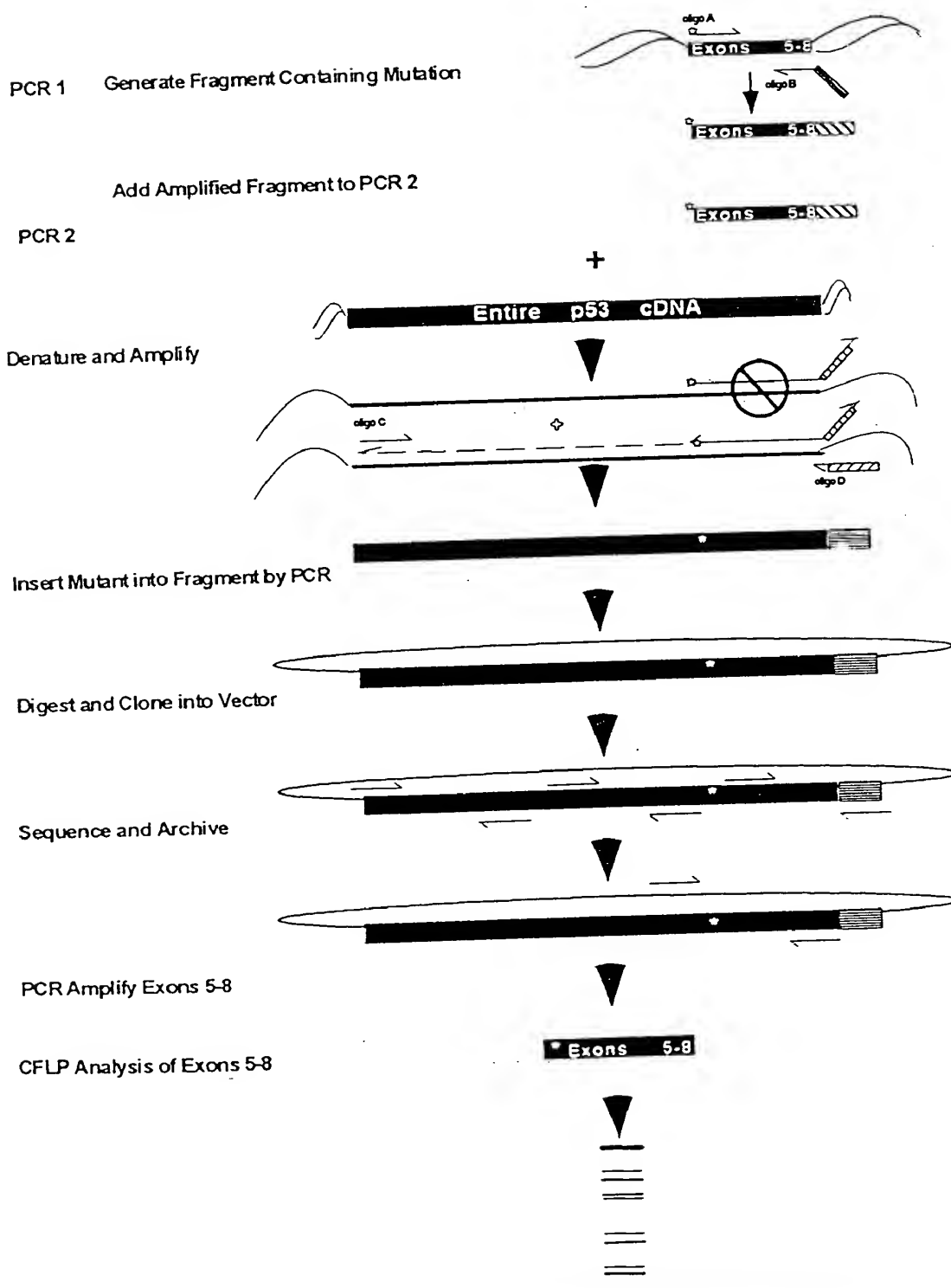


FIGURE 78

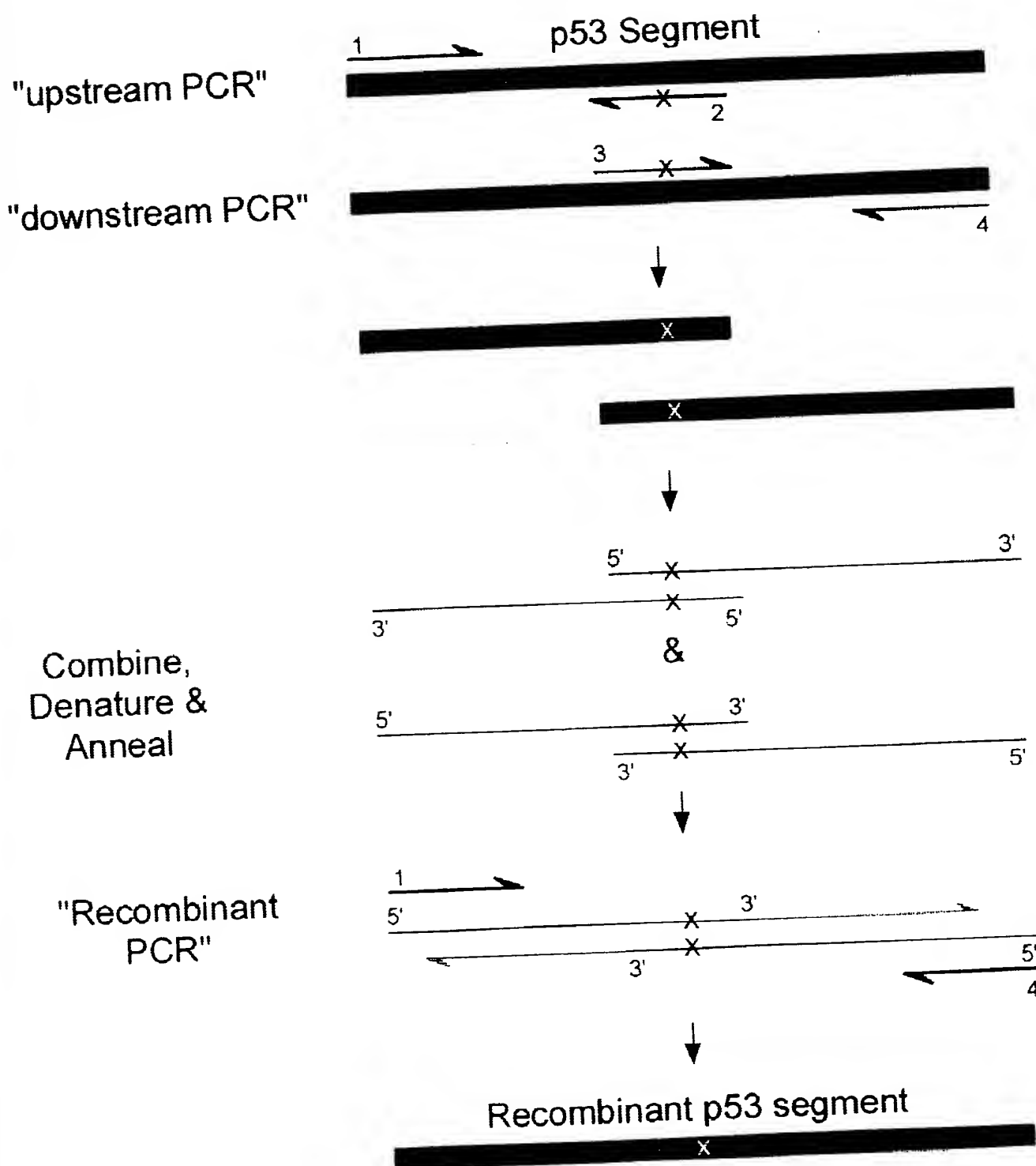


FIGURE 79

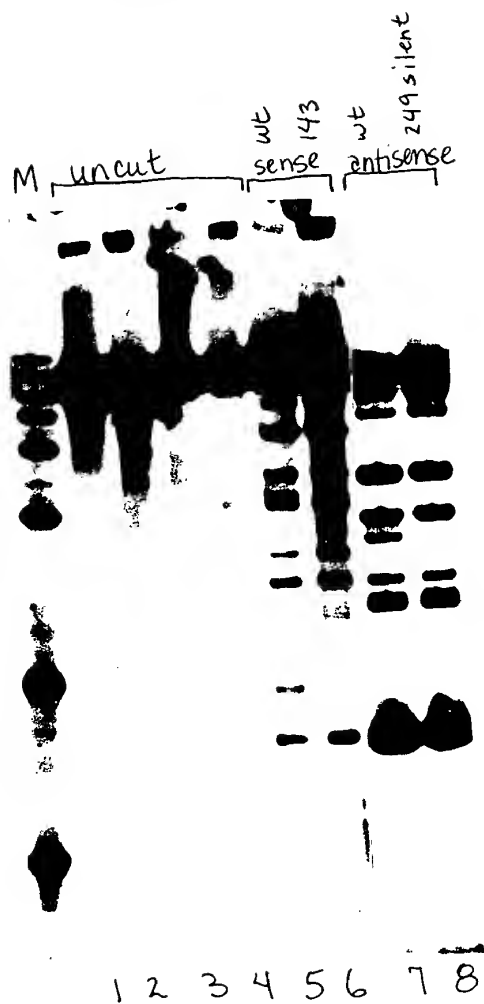


FIGURE 80

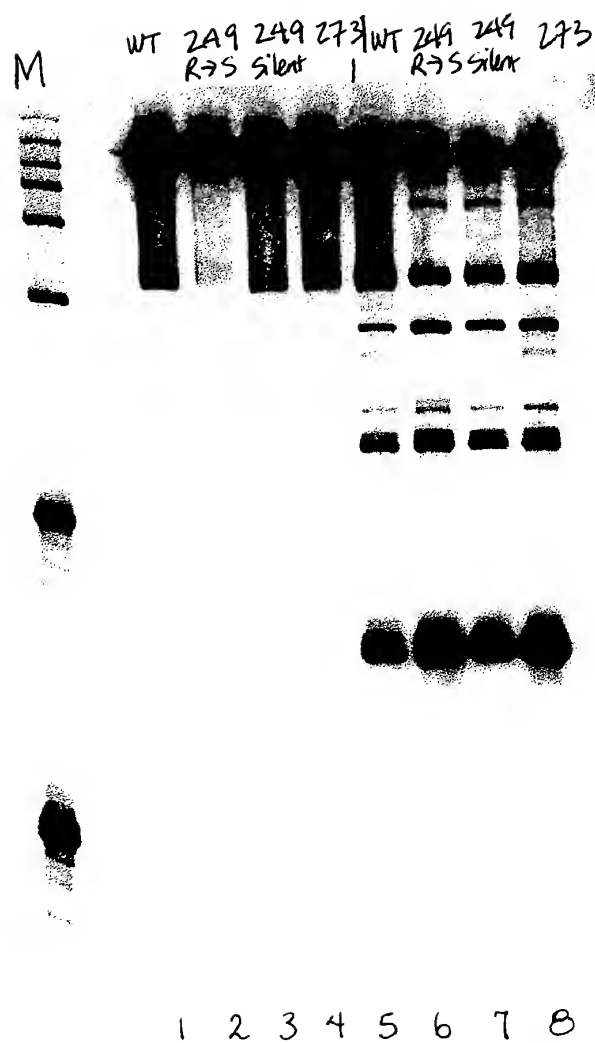


FIGURE 82

HCV1.1	(SEQ ID NO:121)	1	CTGTCTTTCAC	GCAGAAAGCG	TCTGGCCATG	GCGTTAGTAT	GAGTGTGCTG	50
HCV2.1	(SEQ ID NO:122)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTGCTG	
HCV3.1	(SEQ ID NO:123)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTGCTG	
HCV4.2	(SEQ ID NO:124)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTGCTG	
HCV6.1	(SEQ ID NO:125)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTGCTG	
HCV7.1	(SEQ ID NO:126)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTGCTG	
HCV1.1		51	CAGCCTCCAG	GACCCCCCTT	CCCGGAGAG	CCATAGTGGT	CTGCGGAACC	100
HCV2.1			CAGCCTCCAG	GACCCCCCTT	CCCGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV3.1			CAGCCTCCAG	GACCCCCCTT	CCCGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV4.2			CAGCCTCCAG	GACCCCCCTT	CCCGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV6.1			CAGCCTCCAG	GACCCCCCTT	CCCGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV7.1			CAGCCTCCAG	GACCCCCCTT	CCCGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV1.1		101	GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGTCCCTTTC	TTGGAT-AAA	150
HCV2.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGTCCCTTTC	TTGGAT-CAA	
HCV3.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGTCCCTTTC	TTGGAT-CAA	
HCV4.2			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGTCCCTTTC	TTGGAT-CAA	
HCV6.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGTCCCTTTC	TTGGAT-CAA	
HCV7.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGTCCCTTTC	TTGGAT-CAA	
HCV1.1		151	CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	200
HCV2.1			CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV3.1			CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV4.2			CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV6.1			CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV7.1			CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV1.1		201	AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	250
HCV2.1			AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV3.1			AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV4.2			AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV6.1			AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV7.1			AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV1.1		251	GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC	282	
HCV2.1			GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV3.1			GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV4.2			GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV6.1			GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV7.1			GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		

FIGURE 83

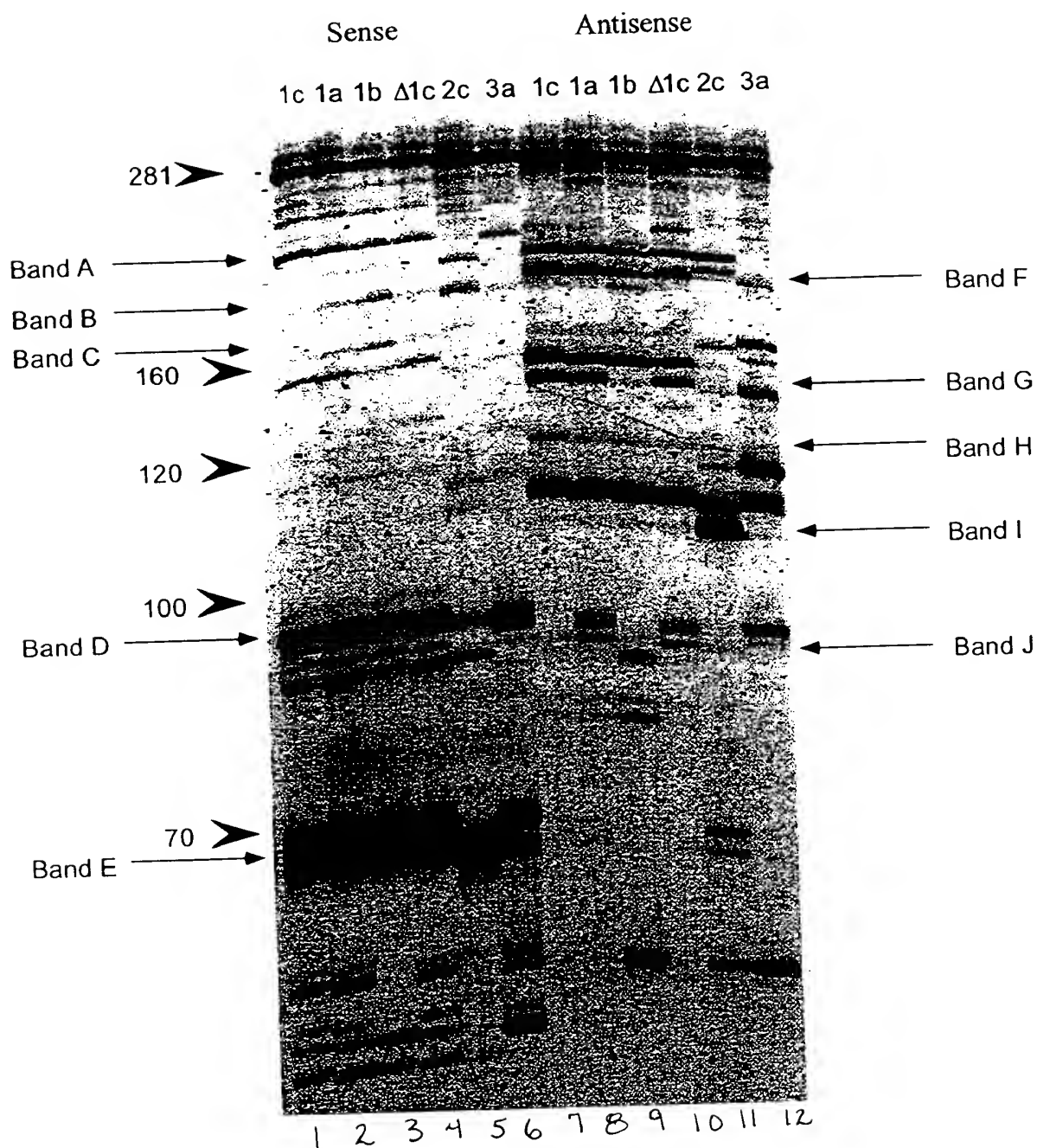


FIGURE 84

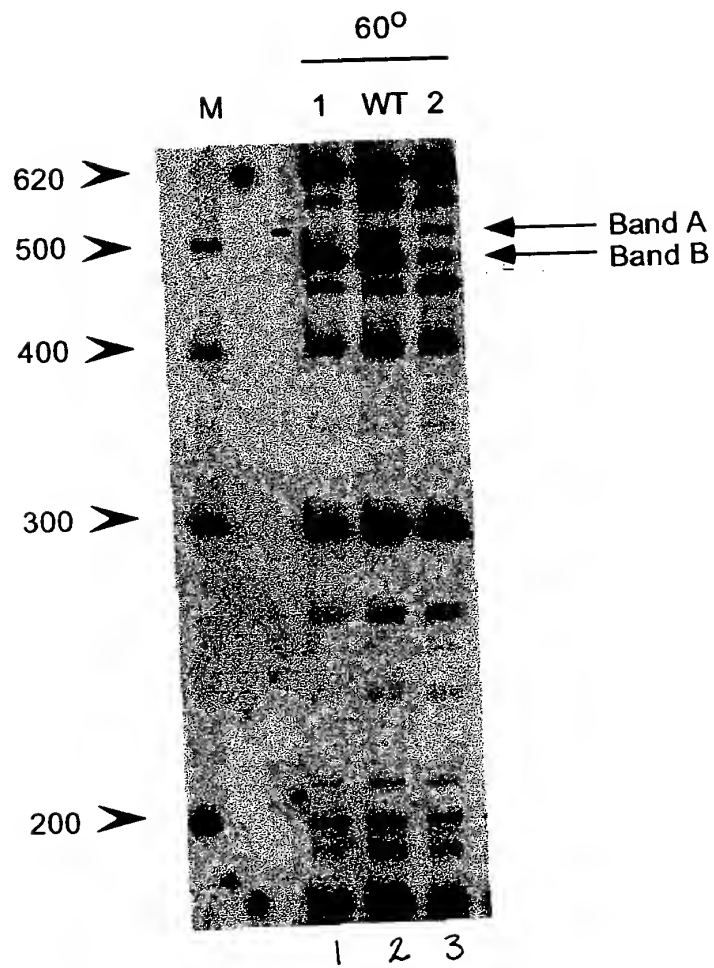


FIGURE 85

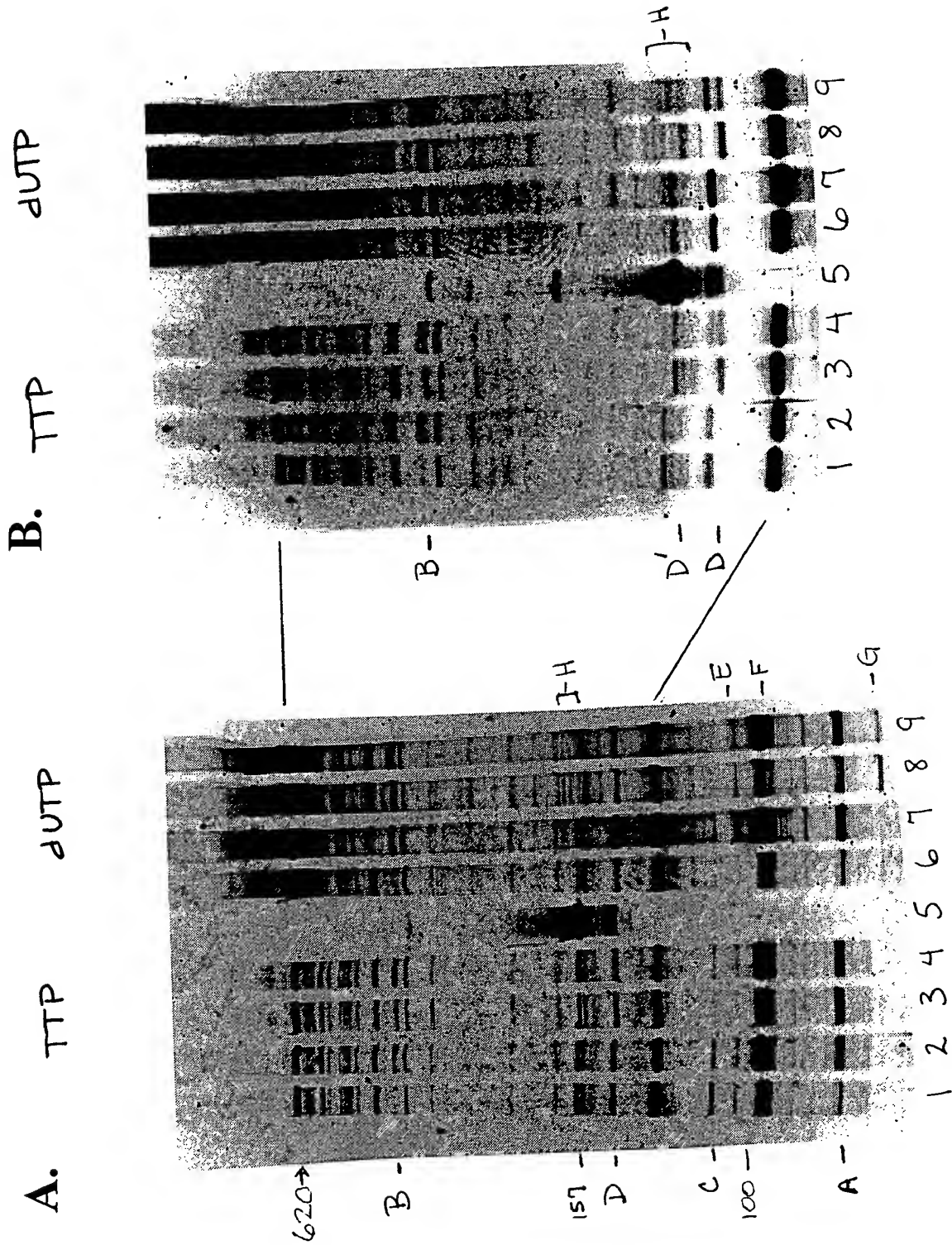


FIGURE 86

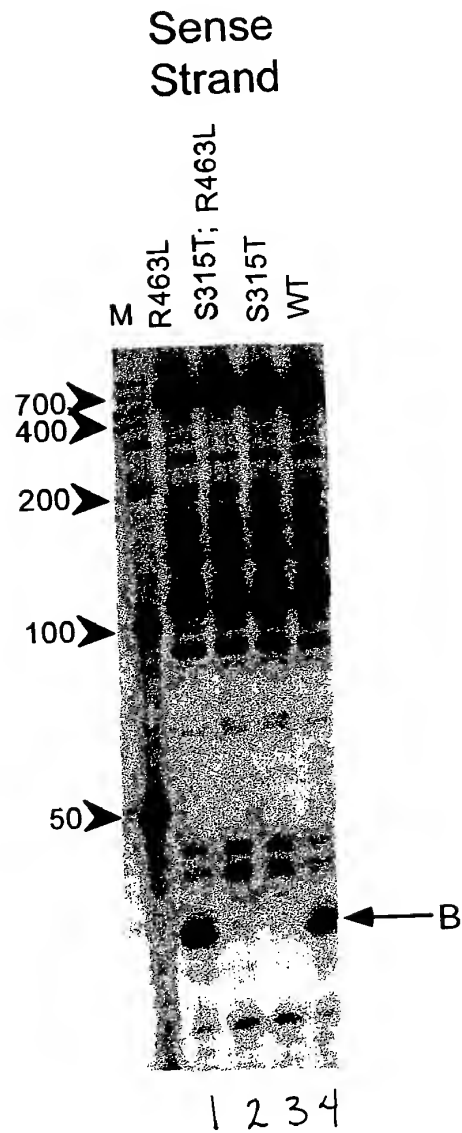
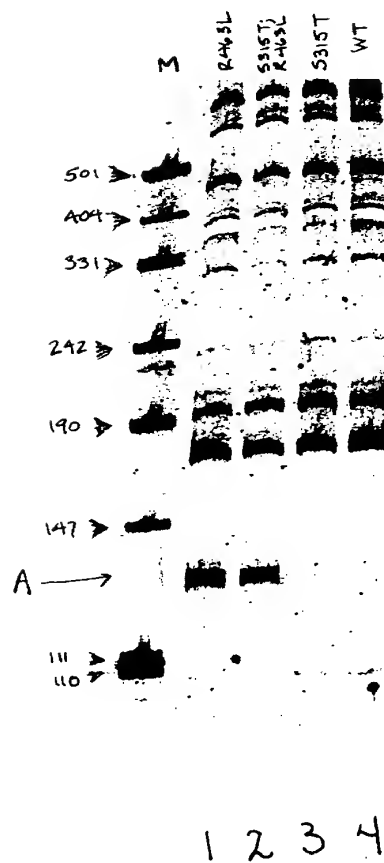


FIGURE 87

Antisense
Strand

10	20	30	40	50	60	1638
AGA GTTTGATCCT GGCTCAG						
AAATTGAAGA	GTTTGATCAT	GGCTCAGATT	GAACGCTGGC	GGCAGGCCTA	ACACATGCAA	
TTTAACTTCT	CAAAC TAGTA	CCGAGTCTAA	CTTGCGACCG	CCGTCCGGAT	TGTGTACGTT	
70	80	90	100	110	120	ER10
GGCGGAC GGGTGAGTAA						
GTCGAACGGT	AACAGGAAGA	AGCTTGCTTC	TTTGCTGACG	AGTGGCGGAC	GGGTGAGTAA	
CAGCTTGCCA	TTGTCCTTCT	TCGAACGAAG	AAACGACTGC	TCACCGCCTG	CCCACTCATT	
130	140	150	160	170	180	
TGTCTGGGAA	ACTGCCTGAT	GGAGGGGGAT	AACTACTGGA	AACGGTAGCT	AATACCGCAT	
ACAGACCCCT	TGACGGACTA	CCTCCCCCTA	TTGATGACCT	TTGCCATCGA	TTATGGCGTA	
190	200	210	220	230	240	
AACGTCGCAA	GACCAAAGAG	GGGGACCTTC	GGGCCTCTTG	CCATCGGATG	TGCCCAGATG	
TTGCAGCGTT	CTGGTTTCTC	CCCCTGGAAG	CCCGGAGAAC	GGTAGCCTAC	ACGGGTCTAC	
250	260	270	280	290	300	
GGATTAGCTA	GTAGGTGGGG	TAACGGCTCA	CCTAGGCGAC	GATCCCTAGC	TGGTCTGAGA	
CCTAATCGAT	CATCCACCCC	ATTGCCGAGT	GGATCCGCTG	CTAGGGATCG	ACCAGACTCT	
310	320	330	340	350	360	
GGATGACCAG	CCACACTGGA	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTGG	
CCTACTGGTC	GGTGTGACCT	TGACTCTGTG	CCAGGTCTGA	GGATGCCCTC	CGTCGTCACC	
TGA GGATGCCCTC CGTCGTC						1659
370	380	390	400	410	420	
GGAATATTGC	ACAATGGGCG	CAAGCCTGAT	GCAGCCATGC	CGCGTGTATG	AAGAAGGCCT	
CCTTATAACG	TGTTACCCGC	GTTCCGACTA	CGTCGGTACG	GCGCACATAC	TTCTTCCGGA	
430	440	450	460	470	480	
TCGGGTTGTA	AAGTACTTTC	AGCGGGGAGG	AAGGGAGTAA	AGTTAATACC	TTTGCTCATT	
AGCCCAACAT	TTCATGAAAG	TCGCCCCCTC	TTCCCTCATT	TCAATTATGG	AAACGAGTAA	
490	500	510	520	530	540	
GACGTTACCC	GCAGAAGAAG	CACCGGCTAA	CTCCGTGCCA	GCAGCCGCGG	TAATACGGAG	
CTGCAATGGG	CGTCTTCTTC	GTGGCCGATT	GAGGCACGGT	CGTCGGCGCC	ATTATGCCTC	
550	560	570	580	590	600	
GGTGCAAGCG	TTAATCGGAA	TTACTGGGCG	TAAAGCGCAC	GCAGGCGGTT	TGTTAAGTCA	
CCACGTTCCG	AATTAGCCTT	AATGACCCGC	ATTTGCGGTG	CGTCCGCCAA	ACAATTCACT	
610	620	630	640	650	660	
GATGTGAAAT	CCCCGGGCTC	AACCTGGGAA	CTGCATCTGA	TACTGGCAAG	CTTGAGTCTC	
CTACACTTTA	GGGGCCCGAG	TTGGACCCTT	GACGTAGACT	ATGACCGTTC	GAACCTCAGAG	
670	680	690	700	710	720	
GTAGAGGGGG	GTAGAATTCC	AGGTGTAGCG	GTGAAATGCG	TAGAGATCTG	GAGGAATACC	
CATCTCCCCC	CATCTTAAGG	TCCACATCGC	CACTTTACGC	ATCTCTAGAC	CTCCTTATGG	
730	740	750	760	770	780	
GGTGCGAAG	GCGGCCCCCT	GGACGAAGAC	TGACGCTCAG	GTGCGAAAGC	GTGGGGAGCA	
CCACCGCTTC	CGCCGGGGGA	CCTGCTTCTG	ACTGCGAGTC	CACGCTTTCG	CACCCCTCGT	

790 800 810 820 830 840
AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT GTCGACTTGG AGGTTGTGCC
TTGTCCTAAT CTATGGGACC ATCAGGTGCG GCATTTGCTA CAGCTGAACC TCCAACACGG

850 860 870 880 890 900
CTTGAGGCGT GGCTTCCGGA GCTAACGCGT TAAGTCGACC GCCTGGGGAG TACGGCCGCA
GAACTCCGCA CCGAAGGCCT CGATTGCGCA ATTCAGCTGG CGGACCCCTC ATGCCGGCGT

910 920 930 940 950 960
AGGTTAAAAC TCAAATGAAT TGACGGGGGC CCGCACAAGC GGTGGAGCAT GTGGTTTAAT
TCCAATTTTG AGTTTACTTA ACTGCCCCCG GCGTGTTTCG CCACCTCGTA CACCAAATTA

970 980 990 1000 1010 1020
TCGATGCAAC GCGAAGAACC TTACCTGGTC TTGACATCCA CGGAAGTTTT CAGAGATGAG
AGCTACGTTG CGCTTCTTGG AATGGACCAG AACTGTAGGT GCCTTCAAAA GTCTCTACTC

1030 1040 1050 1060 1070 1080
AATGTGCCTT CGGGAACCGT GAGACAGGTG CTGCATGGCT GTCGTCAGCT CGTGTGTGA
TTACACGGAA GCCCTTGGCA CTCTGTCCAC GACGTACCGA CAGCAGTCGA GCACAACACT

1090 1100 1110 1120 1130 1140
GC AACGAGCGCA ACCC
AATGTTGGGT TAAGTCCCGC AACGAGCGCA ACCCTTATCC TTTGTTGCCA GCGGTCCGGC
TTACAACCCA ATTCAGGGCG TTGCTCGCGT TGGGAATAGG AAACAACGGT CGCCAGGCCG

1150 1160 1170 1180 1190 1200
ATG ACGTCAAGTC
ATG ACGTCAAGTC
CGGGAACTCA AAGGAGACTG CCAGTGATAA ACTGGAGGAA GGTGGGGATG ACGTCAAGTC
GCCCTTGAGT TTCCTCTGAC GGTCACTATT TGACCTCCTT CCACCCCTAC TGCAGTTTACG

1210 1220 1230 1240 1250 1260
ATCATGGCCC TTA
ATCATGGCCC TTACGA
ATCATGGCCC TTACGACCAG GGCTACACAC GTGCTACAAT GGCGCATACA AAGAGAAGCG
TAGTACCGGG AATGCTGGTC CCGATGTGTG CACGATGTTA CCGCGTATGT TTCTCTTCGC

1270 1280 1290 1300 1310 1320
ACCTCGCGAG AGCAAGCGGA CCTCATAAAG TGCGTCGTAG TCCGGATTGG AGTCTGCAAC
TGGAGCGCTC TCGTTCGCCT GGAGTATTTT ACGCAGCATC AGGCCTAACC TCAGACGTTG

1330 1340 1350 1360 1370 1380
TCGACTCCAT GAAGTCGGAA TCGCTAGTAA TCGTGATCA GAATGCCACG GTGAATACGT
AGCTGAGGTA CTTACGCCTT AGCGATCATT AGCACCTAGT CTTACGGTGC CACTTATGCA
GC CACTTATGCA

1390 1400 1410 1420 1430 1440
TCCCGGGCCT TGTAACACACC GCCCGTCACA CCATGGGAGT GGGTTGCAAA AGAAGTAGGT
AGGGCCCCGA ACATGTGTGG CGGGCAGTGT GGTACCCTCA CCAACGTTT TCTTCATCCA

1450 1460 1470 1480 1490 1500
AGCTTAACTT TCGGGAGGGC GCTTACCACT TTGTGATTCA TGACTGGGGT GAAGTCGTAA
TCGAATTGGA AGCCCTCCCG CGAATGGTGA AACACTAAGT ACTGACCCCA CTTACAGCAT

1510 1520 1530 1540 1550
CAAGGTAACC GTAGGGGAAC CTGCGGTTGG ATCACCTCCT TA.....
GTTCCATTGG CATCCCCCTG GACGCCAACC TAGTGGAGGA AT.....

SB-1

SB-3
SB-4

SB-3
SB-4

1743

1743

FIGURE 89

Sheet 1/3

1638 (SEQ ID NO:151)
 E.colirrsE (SEQ ID NO:158) 0 ...AAATTGAAGAGTTTGATCATGGCTCAGATTGAA CGCTGGCGGCGAGCCCTAACACATGCA
 Cam.jejun5 (SEQ ID NO:159) 0 ~TTTTATGGAGAGTTGATCCTGGCTCAGAGTGAA CGCTGGCGGCGTGCCTAATACATGCA
 Stp.aureus (SEQ ID NO:160) 0 ..TTTTATGGAGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCCTAATACATGCA

AGAGTTTGATCCTGGCTCAG

ER10 (SEQ ID NO:152)
 E.colirrsE
 Cam.jejun5
 Stp.aureus

60 AGTCGAACGGTAAACAG-----GAAGAAGCTTGCTTCTTT-----GCTGACGAGTGGCGGACGGG
 62 AGTCGAACGAT-----GAAGCTTCTAGCTTGCTAGAGTGGA-----TTAGTGGCGCACGGG
 61 AGTCGAGCGAA-----CGGACGAGAAGCTTGCTTCTCTGATG-----TT-AGCGGCGGACGGG

GGCGGACGGG

ER10
 E.colirrsE
 Cam.jejun5
 Stp.aureus

114 TGAGTAATGTCTGGGA-AACTGCCGTGATGGAGGGGATACTACTGGAACCGGTAGCTAATA
 114 TGAGTAAGGTATAGTTAATCTGCCCTACACAAGAGGACAAACAGTTGGAAACGACTGTCTAATA
 113 TGAGTAACACGCTGGATAACCTACCTATAAGACTGGGATAACTTCGGGAAACCGGAGACTAATA

TGAGTAA

E.colirrsE
 Cam.jejun5
 Stp.aureus

175 CCGCATAAC-----GTCGCAAGAC-----CAAAGAGGGGACCTTCG-GGCCTCTTG
 176 CTCTATACTCTGCTTAAACACAAGTTGAGTAGG-GAAG-----TTTTT-----CG
 175 CCGGATAATATTTTGAACCGCATGGTTCAAAAGTGAAAGACGGT-----CTT-----GCTGTCA

E.colirrsE
 Cam.jejun5
 Stp.aureus

221 CCATCGGATGCCCCAGATGGGATTAGCTAGTAGTGGGTAAACGGCTCACCTAGGCGACGA
 221 GTGTAGGATGAGACTATATAGTATCAGCTAGTTGGTAAGTAATGGCTTACCAAGGCTATGA
 229 CTTATAGATGGATCCGCGCTGCATTAGCTAGTTGGTAAGTTAACGGCTTACCAAGGCAACGA

E.colirrsE
 Cam.jejun5
 Stp.aureus

283 TCCCTAGTGTCTGAGAGGATGACCAAGGATGAGTGGGTAAACGGTCCAGACTCCTA
 283 CGCTTAACTGCTGTGAGAGGATGATCAGTCACTGAACTGAGACACGGTCCAGACTCCTA
 291 TACGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACCTGAGACACGGTCCAGACTCCTA
 ACTCCTA

E.colirrsE
 Cam.jejun5
 Stp.aureus

345 CCGGAGGCGAGCAGTGGGGAATATTGCACAATGGCGCAAGCCTGATGCAAGCCTGCGCGTG
 345 CCGGAGGCGAGCAGTGGGGAATATTGGCAATGGGGAAACCTGACGCAACCGCGCGTG
 353 CCGGAGGCGAGCAGTGGGGAATCTTCCGCAATGGCGCAAGCCTGACGAGCAACCGCGCGTG
 CCGGAGGCGAGCAG

E.colirrsE
 Cam.jejun5
 Stp.aureus

407 TATGAAGAAGGCCCTTCGGTTGTAAAGTACTTTCAGCGGGGAGGAA-GGGAGTAAAGTTAAT
 407 GAGGATGACACTTTTCGGAGCGTAAACTCTCTTTCTTCTTAGGGAAG-----AATT
 415 AGTGATGAAGGTCTTCGGATCGTAAAACTCTGTATTAGGGAAGAACATATGTGTAAAGTAAAC

E.colirrsE
 Cam.jejun5
 Stp.aureus

468 ACCTTTGCTCATTTGACGTTACCCGCAAGAAAGACCGGTTAACTCGTGCCAGCAGCCGCG
 455 C-----TGACGGTACCTAAGGAATGAACACCGGTTAACTCCGTCCAGCAGCCGCG
 476 -TGTCACATCTTTGACGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCG

<i>E. coli</i> rrsE	530	GTAATACGAGGGTGCAAGCGTTAATCGGAATTACTGGCGGTAAGCGCACGCGCGGTTT
<i>Cam. jej</i> un5	506	GTAATACGAGGGTGCAAGCGTTAATCGGAATCACTGGCGTAAAGGCGCGTAGGCGGATT
<i>Stp. aure</i> s	538	GTAATACGTAGGTGGCAAGCGTTATCCGAATTATTGGCGGTAAGCGCGCGTAGGCGGTTT
<i>E. coli</i> rrsE	592	GTTAAGTCAGATGTGAAATCCCGGGCTCAACCTGGGAACTGCATCTGTACTGTGCAAGCTT
<i>Cam. jej</i> un5	568	ATCAAGTCTCTGTGAAATCTAATGGCTTAACCAATTAAGTCTTGGGAACTGATAGTCTA
<i>Stp. aure</i> s	600	TTTAAGTCTGATGTGAAAGCCCAAGGCTCAACCGTGGAGGGTCATTGGGAACTGGAAAACCTT
<i>E. coli</i> rrsE	654	GAGTCTCGTAGAGGGGGTAGAATCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGA
<i>Cam. jej</i> un5	630	GAGTGAGGGAGAGGCAGATGGAATTTGGTGTAGGGGTAAATCCGTAGATATCACCAAGA
<i>Stp. aure</i> s	662	GAGTGCAGAAAGAGAAAGTGGAAATTCATGTGTAGCGGTGAAATGCGCAGAGATATGGAGGA
<i>E. coli</i> rrsE	716	ATACCGGTGGCGAAGCGGCCCTTGACGAAGACTGACGCTCAGGTGCGAAACGCTGGGGA
<i>Cam. jej</i> un5	692	ATACCCATTGCGAAGCGCATCTGTGGAACTCAACTGACGTAAGCGCGAAAGCGTGGGGA
<i>Stp. aure</i> s	724	ACACAGTGGCGAAGCGGACTTCTGTCTGTAACTGACGCTGATGTGCGAAAGCGCTGGGGA
<i>E. coli</i> rrsE	778	GCAAAACAGGATTAGATACCTTGTTAGTCCAGCGCGTAAACGATGTCGACTTGGAGGTTGTGC
<i>Cam. jej</i> un5	754	GCAAAACAGGATTAGATACCTTGTTAGTCCAGCGCGTAAACGATGTCGACTTGTGGGGT
<i>Stp. aure</i> s	786	TCAAAACAGGATTAGATACCTTGTTAGTCCAGCGCGTAAACGATGTCGACTTGTAGGGG
<i>E. coli</i> rrsE	840	C-CTTGA-GGCGTGGCTTCCGGAGCTAACCGCTTAAGTCGACCGCTGGGAGTACGGCCGC
<i>Cam. jej</i> un5	816	G-CTAGT-CATCTCAGTAATGCAGCTAACCGATTAAGTGTACCGCTGGGAGTACGGTCCG
<i>Stp. aure</i> s	848	GT-TTCCGCCCTTAGTGCTGCAGCTAACCGATTAAGCACTCCGCCCTGGGAGTACGACCGC
<i>E. coli</i> rrsE	900	AAGGTTAAAACTCAAATGAATTGACGGGGGCCGCAACAGCGGTGGAGCATGTGGTTTAATT
<i>Cam. jej</i> un5	876	AAGATTAAAACTCAAAGGAATAGACGGGGACCCGCAACAGCGGTGGAGCATGTGGTTTAATT
<i>Stp. aure</i> s	909	AAGTTGAAACTCAAAGGAATTGACGGGGACCCGCAACAGCGGTGGAGCATGTGGTTTAATT
<i>E. coli</i> rrsE	962	CGATGCAACGCGAAGAACCTTACCTGGTCTTGACATCCACGGAAGTTTTCAGAGATGAGAAT
<i>Cam. jej</i> un5	938	CGAAGATACGGAAGAACCTTACCTGGCTTGATATCCTAAGAACCTTTTAGAGATAAGAGG
<i>Stp. aure</i> s	971	CGAAGCAACGCGAAGAACCTTACCAATCTTGACATCCTTTGACAACTCTAGAGATAGAGCC
<i>E. coli</i> rrsE	1024	GTG--CCTTCGGG--AA-CCGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTGTGA
<i>Cam. jej</i> un5	1000	GTGCTAGCTTGCTAGAA-CTTAGAGACAGGTGCTGACGGCTGTCGTCAGCTCGTGTGTGA
<i>Stp. aure</i> s	1033	TTCC-CCTTCGGG--GGACAAAGTAGACAGGTGGTGCATGGTGTGTCGTCAGCTCGTGTGTGA
SB-1		GCAACGAGCGCAACCC
<i>E. coli</i> rrsE	1081	AATGTTGGGTTAAGTCCCGCAACAGCGCAACCTTATCTTTGTTGCCAGCGGTCCGG-CC
<i>Cam. jej</i> un5	1061	GATGTTGGGTTAAGTCCCGCAACAGCGCAACCTTATCTTTGTTGCCAGCGGTCCGG-CC
<i>Stp. aure</i> s	1092	GATGTTGGGTTAAGTCCCGCAACAGCGCAACCTTAAAGCTTAGTTGCCATCA-TTAAGT-T

FIGURE 89

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SB-3 (SEQ ID NO:157) ATGACGTCAAGTCATC
 SB-4 (SEQ ID NO:154) ATGACGTCAAGTCATC
 E.colirrsE 1142 GGAACCTCAAAGGAGCTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATC
 Cam.jejun5 1122 GAGCACTCTAAATAGACTGCTTTCG-TAAGGAGGAGGAAGGTGGGACGACGTCAAGTCATC
 Stp.aureus 1152 GGGCACTCTAAGTTGACTTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAATCATC

SB-3 ATGGCCCTTA
 SB-4 ATGGCCCTTACGA
 E.colirrsE 1204 ATGGCCCTTACGACAGGGCTACACACGTGCTACAATGGCGCATACAAAGAGAAGCGACCTC
 Cam.jejun5 1183 ATGGCCCTTATGCCAGGGCGACACACGTGTACAATGGCAATACAAAGGGCAGCGAAACC
 Stp.aureus 1214 ATGGCCCTTATGATTTGGGCTACACACGTGTACAATGGCAATACAAAGGGCAGCGAAACC

E.colirrsE 1266 GCGAGAGCAAGCGGACCTCATAAAGTCGTGCTAGTCCGGATTGGAGTCTGCAACTCGACTC
 Cam.jejun5 1245 GCGAGGTGGAG-CAAAATCTATAAAATATGTCCTCCAGTTCGGATTGTTCTCTGCAACTCGAGAG
 Stp.aureus 1276 GCGAGGTCAAGCAAAATCCCATAAAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTA

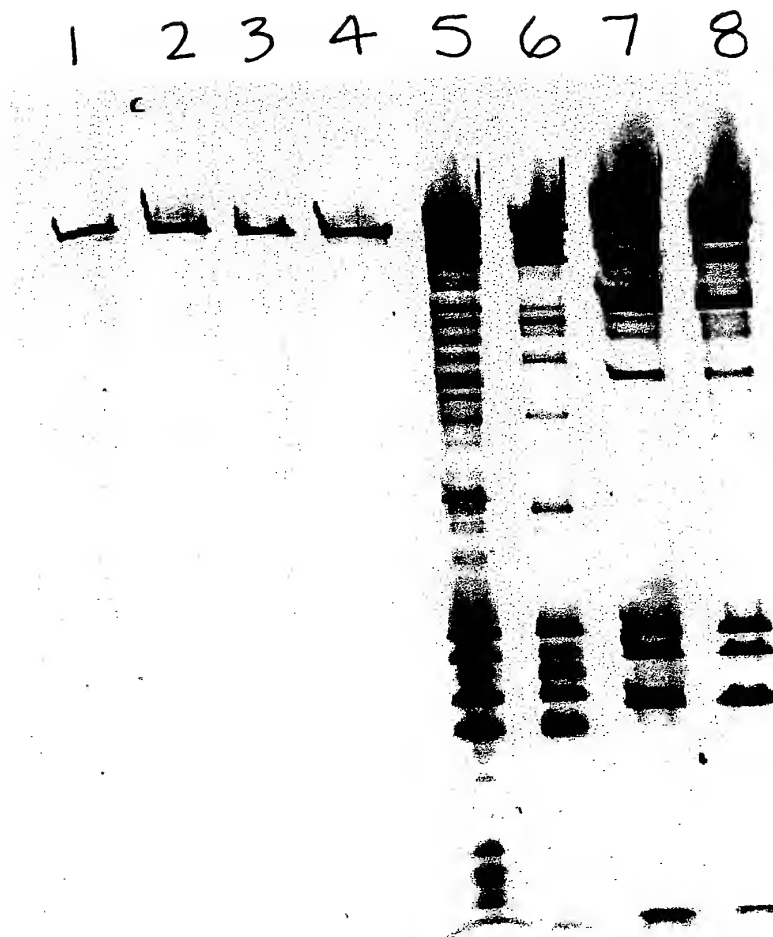
E.colirrsE 1328 CATGAAGTCGGAATCGCTAGTAATCGTGGATCAGA-ATGCCACGGTGAATA CGTTCCTCGGGC
 Cam.jejun5 1306 CATGAAGCCGGAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTGAATACGTTCCCGGGT
 Stp.aureus 1338 CATGAAGCTGGAATCGCTAGTAATCGTAGATCAGC-ATGCTACGGTGAATACGTTCCCGGGT
 1743 (compl) CGGTGAATACGTTCCCGGGC

E.colirrsE 1389 CTTGTACACACCGCCCGTCAACCATGGGAGTGGTTGCAAAAGAGTAGGTAGCTTAACCT
 Cam.jejun5 1368 CTTGTACTACCGCCCGTCAACCATGGGAGTTGATTTCACTCGAAGCCGGAATACT--A-A
 Stp.aureus 1399 ATTGTACACACCGCCCGTCAACCATGGGAGTTTGTAAACACCCGGAAGCCGGTGGAGTAACCT
 1743 (compl) CTTGTAC

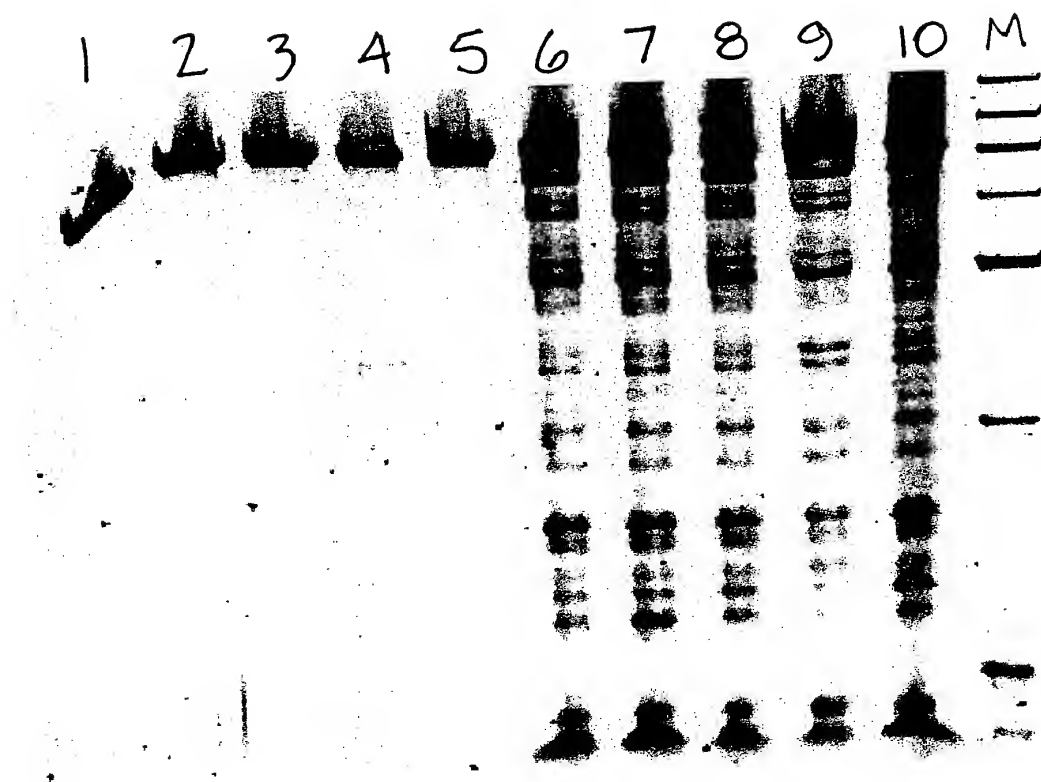
E.colirrsE 1451 TCG-GGAGGGCGCTTACCACCTTTGTGATTATGACTGGGGTGAAGTCGTAAACAAGGTAACCG
 Cam.jejun5 1427 AC---T-AGTTACCGTCCACAGTGGAAATCAGCGACTGGGGTGAAGTCGTAAACAAGGTAACCG
 Stp.aureus 1461 TTTAGGAGCTAGCCGTCGAAGGTGGGACAAATGATTGGGGTGAAGTCGTAAACAAGGTAACCG

E.colirrsE 1512 TAGGGGAACCTGCGGTTGGATCACCTCCTTA---
 Cam.jejun5 1485 TAGGAGAACCTGCGGTTGGATCACCTCCT-----
 Stp.aureus 1523 TATCGGAAGGTGCGGCTGGATCACCTCCTTTCT-

FIGURE 90



A.



B.

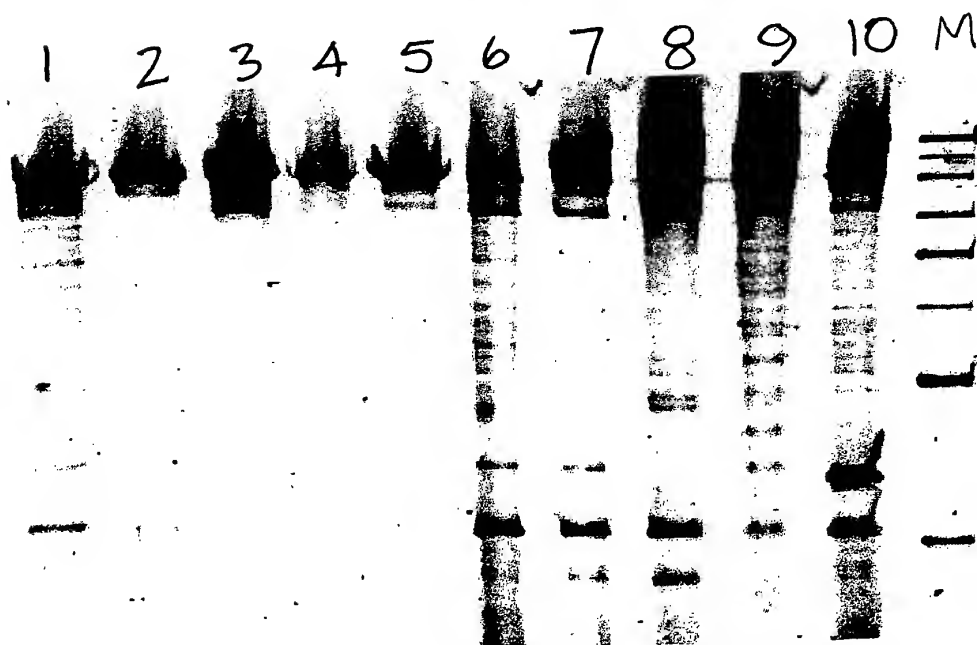


FIGURE 92

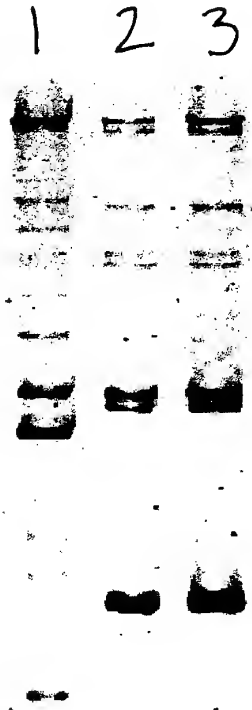


FIGURE 93



FIGURE 94

